



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Burton, Dennis R  
Barbas, Carlos F  
Lerner, Richard A
- (ii) TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TO HUMAN IMMUNODEFICIENCY VIRUS
- (iii) NUMBER OF SEQUENCES: 170
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel
  - (B) STREET: 10666 North Torrey Pines Road, Suite 220,  
Mail Drop TPC8
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/899,575
  - (B) FILING DATE: 24-JUL-1997
  - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/276,852
  - (B) FILING DATE: 18-JUL-1994
  - (A) APPLICATION NUMBER: US 08/178,302
  - (B) FILING DATE: 30-SEP-1993
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/954,148
  - (B) FILING DATE: 30-SEP-1992
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Fitting, Thomas
  - (B) REGISTRATION NUMBER: 34,163
  - (C) REFERENCE/DOCKET NUMBER: TSRI 313.2
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619-554-2937
  - (B) TELEFAX: 619-554-6312

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCGCAAAT TCTATTTCAA GGAGACAGTC ATAATGAAAT ACCTATTGCC TACGGCAGCC	60
GCTGGATTGT TATTACTCGC TGCCCAACCA GCCATGGCCC AGGTGAAACT GCTCGAGATT	120
TCTAGACTAG TTACCCGTAC GACGTTCCGG ACTACGGTTC TTAATAGAAT TCG	173

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCGACGAAAT CTATTAAGAA CCGTAGTCCG GAACGTCGTA CGGGTAACTA GTCTAGAAAT	60
CTCGAGCACT TTCACCTGGG CCATGGCTGG TTGGGCAGCG AGTAATAACA ATCCAGCGGC	120
TGCCGTAGGC AATAGGTATT TCATTATGAC TGTCTCCTTG AAATAGAATT TGC	173

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAATTCTAA ACTAGTCGCC AAGGAGACAG TCATAATGAA ATACCTATTG CCTACGGCAG	60
CCGCTGGATT GTTATTACTC GCTGCCCAAC CAGCCATGGC CGAGCTCGTC AGTTCTAGAG	120
TTAAGCGGCC G	131

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCGACGGCCG CTAACTCTA GAACTGACGA GCTCGGCCAT GGCTGGTTGG GCAGCGAGTA	60
ATAACAATCC AGCGGCTGCC GTAGGCAATA GGTATTTTCAT TATGACTGTC TCCTTGGCGA	120
CTAGTTTAGA ATTCAAGCT	139

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala
1				5					10					15	

Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu
			20					25	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala
1				5					10					15	

Ala	Gln	Pro	Ala	Met	Ala	Glu
						20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAAATTTCA	60
CACAGGAGGA AGGATCCATG AAATACCTAT TGCCTACGGC AGCCGCTGGA TTGTTATTAC	120
TCGCTGCCCCA ACCAGCCATG GCCGAGCTCG GTCGGTCGGT CCTCGAGGGT CGGTCGGTCT	180
CTAGAGTTAA GCGGCCGC	198

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGGCCGCTT AACTCTAGAG ACCGACCGAC CCTCGAGGAC CGACCGACCG AGCTCGGCCA	60
TGGCTGGTTG GGCAGCGAGT AATAACAATC CAGCGGCTGC CGTAGGCAAT AGGTATTTC	120
TGGATCCTTC CTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAT TATACGAGCC	180
GATGATTAAT TGTCAACA	198

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Thr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
1                    5                    10                    15  
  
Ala Gln Pro Ala Met Ala Glu Leu  
                    20

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 220 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAAATTTC          60  
CACAGGAGGA AGGATCCATG AAATACCTAT TGCCTACGGC AGCCGCTGGA TTGTTATTAC          120  
TCGCTGCCCA ACCAGCCATG GCCCAGGTGA AACTGCTCGA GGGTCGGTCG GTCTCTAGAC          180  
GGTCGGTCGG TCACTAGTCA TCATCATCAT CATTAAGCTA                                  220

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 220 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGCTTAATG ATGATGATGA TGACTAGTGA CCGACCGACC GTCTAGAGAC CGACCGACCC	60
TCGAGCAGTT TCACCTGGGC CATGGCTGGT TGGGCAGCGA GTAATAACAA TCCAGCGGCT	120
GCCGTAGGCA ATAGGTATTT CATGGATCCT TCCTCCTGTG TGAAATTGTT ATCCGCTCAC	180
AATTCCACAC ATTATACGAG CCGATGATTA ATTGTCAACA	220

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Lys	Thr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Ala
1				5					10				15	

Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Leu	Glu
		20					25				

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Ser His His His His His  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCCGCAAAT TCTATTTCAA GGAGACAGTC AT

32

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATT

36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTTATTACTC GCTGCCCAAC CAGCCATGGC CC

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGTTTCACC TGGGCCATGG CTGGTTGGG

29

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGCGAGTAA TAACAATCCA GCGGCTGCCG TAGGCAATAG

40

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTATTTTCATT ATGACTGTCT CCTTGAAATA GAATTTGC

38

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGGTGAAACT GCTCGAGATT TCTAGACTAG TTACCCGTAC

40

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGAACGTCG TACGGGTAAC TAGTCTAGAA ATCTCGAG

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACGTTCCGG ACTACGGTTC TTAATAGAAT TCG

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCGACGAATT CTATTAAGAA CCGTAGTC

28

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGAATTCTAA ACTAGTCGCC AAGGAGACAG TCAT

34

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATT

36

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTTATTACTC GCTGCCCAAC CAGCCATGGC C

31

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAGCTCGTCA GTTCTAGAGT TAAGCGGCCG

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTATTTTCATT ATGACTGTCT CCTTGGCGAC TAGTTTAGAA TTCAAGCT

48

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGCGAGTAA TAACAATCCA GCGGCTGCCG TAGGCAATAG

40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGACGAGCTC GGCCATGGCT GGTGGG

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCGACGGCCG CTTAACTCTA GAAC

24

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCATTCGTTT GTGAATATCA AGGCCAAGGC CAATCGTCTG ACCTGCCTCA ACCTCCTGTC	60
AATGCTGGCG GCGGCTCTGG TGGTGGTTCT GGTGGCGGCT CTGAGGGTGG TGGCTCTGAG	120
GGTGGCGGTT CTGAGGGTGG CGGCTCTGAG GGAGGCGGTT CCGGTGGTGG CTCTGGTTCC	180
GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC	240
GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAAC TTG ATTCTGTCGC TACTGATTAC	300
GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTCCGGCC TTGCTAATGG TAATGGTGCT	360
ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA	420
CCTTTAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC	480
CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC	540
TTATTCGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG	600
TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GGTATTCCGT	660
TATTAT	666

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro	Phe	Val	Cys	Glu	Tyr	Gln	Gly	Gln	Gly	Gln	Ser	Ser	Asp	Leu	Pro	1	5	10	15
Gln	Pro	Pro	Val	Asn	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	20	25	30	
Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	35	40	45	
Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	50	55	60	
Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	65	70	75	80
Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	Asp	Ser	Val	85	90	95	
Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	Gly	Asp	Val	Ser	100	105	110	
Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	Phe	Ala	Gly	Ser	Asn	115	120	125	
Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	Asn	Ser	Pro	Leu	Met	Asn	130	135	140	
Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	Pro	Gln	Ser	Val	Glu	Cys	Arg	145	150	155	160
Pro	Phe	Val	Phe	Ser	Ala	Gly	Lys	Pro	Tyr	Glu	Phe	Ser	Ile	Asp	Cys	165	170	175	
Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val	Phe	Ala	Phe	Leu	Leu	Tyr	Val	180	185	190	
Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr	Phe	Ala	Asn	Ile	Leu	Arg	Asn	195	200	205	
Lys	Glu	Ser														210			

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAGACGACTA GTGGTGGCGG TGGCTCTCCA TTCGTTTGTG AATATCAA

48

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTACTAGCTA GCATAATAAC GGAATACCCA AAAGAACTGG

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TATGCTAGCT AGTAACACGA CAGGTTTCCC GACTGG

36

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCGAGCTCG AATTCGTAAT CATGGTC

27

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCTGTTGAA TTCGTGAAAT TGTATCCGC T

31

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGACGACTA GTGGTGGCGG TGGCTCTCCA TTCGTTTGTG AATATCAAGG CCAAGGCCAA	60
TCGTCTGACC TGCCTCAACC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGTTCTGGT	120
GGCGGCTCTG AGGGTGGTGG CTCTGAGGCT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGA	180
GGCGGTTCCG GTGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAAACGCT	240
AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCCG TACAGTCTGA CGCTAAAGGC	300
AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT	360
TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG	420
GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTTACCT	480
TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCATATGAA	540
TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT	600
GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT	660
TAATCATGCC AGTTCTTTTG GGTATTCGGT TATTATGCTA GCTAGTAA	708

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TATGCTAGCT AGTAACACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA GCGCAACGCA	60
ATTAATGTGA GTTAGCTCAC TCATTAGGCA CCCCAGGCTT TACACTTTAT GCTTCCGGCT	120
CGTATGTTGT GTGGAATTGT GAGCGGATAA CAATTCACA CAGGAAACAG CTATGACCAT	180
GATTACGAAT TCGAGCTCGG T	201

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGGTGCAGC TCGAGCAGTC TGGG	24
----------------------------	----

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAGGTGCAGC TCGAGGAGTC TGGG	24
----------------------------	----

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCATGTACTA GTTTTGTAC AAGATTGGG

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GACATCGAGC TCACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAAATTGAGC TCACGCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCGCCGTCTA GAACTAACAC TCTCCCCTGT TGAAGCTCTT TGTGACGGGC AAG

53

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser	Ile	Ser	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Gly
1				5						10	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTCGTTGACC AGGCAGCCCA G

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATAGAAGTTG TTCAGCAGGC A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATTAACCCTC ACTAAAG

17

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCTAAA CTAGCTAGTT CG

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Leu Glu Glu Ser Gly Thr Glu Phe Lys Pro Pro Gly Ser Ser Val Lys  
1 5 10 15

Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Asp Tyr Ala Ser Asn  
20 25 30

Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr  
35 40 45

Ile Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys  
50 55 60

Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Arg Phe Thr Pro Ile Leu  
65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Arg Ile Glu Asp Thr Ala Ile Tyr Tyr  
85 90 95

Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg  
100 105 110

Gly Ala Leu Asp Phe Trp Gly Gln Gly Thr Arg Val Phe Val Ser Pro  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Leu Glu Glu Ser Gly Ala Ala Val Gln Lys Pro Gly Ser Ser Val Arg  
 1 5 10 15

Val Ser Cys Gln Ala Ser Gly Gly Thr Phe Asp Asn Phe Ala Ser Asn  
 20 25 30

Tyr Ala Val Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp  
 35 40 45

Met Gly Gly Ile Thr Pro Thr Ser Gly Thr Ala Thr Tyr Ser Gln Lys  
 50 55 60

Phe Gln Gly Arg Val Thr Ile Ser Ala Ala Pro Leu Thr Pro Ile Ile  
 65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr  
 85 90 95

Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Val  
 100 105 110

Gly Ala Leu Asp Val Trp Gly Gln Gly Thr Thr Val  
 115 120

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Leu Glu Glu Ser Gly Thr Glu Phe Lys Pro Pro Gly Ser Ser Val Lys  
 1                      5                      10                      15  
 Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Asp Tyr Ala Ser Asn  
                     20                      25                      30  
 Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr  
                     35                      40                      45  
 Ile Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys  
                     50                      55                      60  
 Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Arg Phe Thr Pro Ile Leu  
 65                      70                      75                      80  
 Tyr Met Glu Leu Arg Ser Leu Arg Ile Glu Asp Thr Ala Ile Tyr Tyr  
                     85                      90                      95  
 Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg  
                     100                      105                      110  
 Gly Ala Leu Asp Phe Trp Gly Gln Gly Thr Arg Val Phe Val Ser Pro  
                     115                      120                      125

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Leu Glu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
 1                      5                      10                      15  
 Val Ser Cys Lys Ala Ser Gly Gly Ile Phe Ser Asp Phe Ala Ser Asn  
                     20                      25                      30  
 Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr  
                     35                      40                      45  
 Met Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys  
                     50                      55                      60

Phe	Gln	Gly	Arg	Val	Thr	Ile	Ser	Ala	Asp	Ala	Ala	Thr	Pro	Arg	Val
65					70				75					80	
Tyr	Met	Glu	Leu	Arg	Ile	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe
			85					90						95	
Cys	Ala	Arg	Glu	Arg	Arg	Glu	Arg	Gly	Trp	Asn	Pro	Arg	Ala	Leu	Arg
			100					105					110		
Gly	Ala	Leu	Glu	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ile	Val	Ser	Pro
		115				120					125				

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Leu	Glu	Glu	Ser	Gly	Ala	Ala	Val	Gln	Lys	Pro	Gly	Ser	Ser	Val	Arg
1			5					10						15	
Val	Ser	Cys	Gln	Ala	Ser	Gly	Gly	Thr	Phe	Asp	Asn	Phe	Ala	Ser	Asn
			20					25					30		
Tyr	Ala	Val	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp
		35				40					45				
Met	Gly	Gly	Ile	Thr	Pro	Thr	Ser	Gly	Thr	Ala	Thr	Tyr	Ser	Gln	Lys
	50					55				60					
Phe	Gln	Gly	Arg	Val	Thr	Ile	Ser	Ala	Ala	Pro	Leu	Thr	Pro	Ile	Ile
65					70					75				80	
Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Asp	Asp	Asp	Thr	Ala	Val	Tyr	Tyr
				85				90						95	
Cys	Ala	Arg	Glu	Arg	Arg	Glu	Arg	Gly	Trp	Asn	Pro	Arg	Ala	Leu	Val
			100					105					110		
Gly	Ala	Leu	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ile	Val	Ser	Ser
		115				120					125				

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
1                      5                      10                      15

Val Ser Cys Lys Thr Ser Gly Gly Thr Phe Ser Asp Tyr Ala Ser Asn  
                    20                      25                      30

His Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr  
                    35                      40                      45

Met Gly Gly Ile Thr Pro Thr Ser Gly Thr Ala Asp Tyr Ala Gln Lys  
                    50                      55                      60

Phe Gln Ala Arg Val Thr Ile Ser Ala His Glu Phe Thr Pro Ile Val  
65                      70                      75                      80

Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Gln His Ala Thr Tyr Tyr  
                    85                      90                      95

Cys Ala Thr Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg  
                    100                      105                      110

Gly Ala Leu Asp Ile Trp Gly Gln Gly Thr Thr Val Ile Val Ser Ser  
                    115                      120                      125

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg  
1                      5                      10                      15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr  
                   20                                  25                                  30  
 Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
                   35                                  40                                  45  
 Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
                   50                                  55                                  60  
 Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu  
   65                                  70                                  75                                  80  
 Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
                   85                                  90                                  95  
 Thr Lys Tyr Pro Arg Tyr Ser Asp Met Val Thr Gly Val Arg Asn His  
                   100                                  105                                  110  
 Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser  
                   115                                  120                                  125

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Leu Glu Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg  
 1                  5                                  10                                  15  
 Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr  
                   20                                  25                                  30  
 Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
                   35                                  40                                  45  
 Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
                   50                                  55                                  60  
 Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu  
   65                                  70                                  75                                  80  
 Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
                   85                                  90                                  95

Thr Lys Tyr Pro Arg Tyr Phe Asp Met Met Ala Gly Val Arg Asn His  
 100 105 110

Phe Tyr Met Asp Val Trp Gly Thr Gly Thr Thr Val Ile Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr  
 20 25 30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
 35 40 45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu  
 65 70 75 80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
 85 90 95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Ala Gly Val Arg Asn His  
 100 105 110

Leu Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg
1           5           10          15

Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Thr Asn Ser Trp Met Thr
          20           25           30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
          35           40           45

Lys Arg Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
          50           55           60

Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu
65           70           75           80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
          85           90           95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Thr Gly Val Arg Asn His
          100          105          110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1           5           10          15

Leu Ser Cys Glu Ser Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
          20           25           30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
          35           40           45

```

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
 50 55 60  
 Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu  
 65 70 75 80  
 Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
 85 90 95  
 Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Ala Gly Val Arg Asn His  
 100 105 110  
 Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg  
 1 5 10 15  
 Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr  
 20 25 30  
 Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
 35 40 45  
 Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
 50 55 60  
 Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu  
 65 70 75 80  
 Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
 85 90 95  
 Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Thr Gly Val Arg Asn His  
 100 105 110  
 Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1           5           10           15

Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
          20           25           30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
          35           40           45

Lys Ser Lys Phe Asp Gly Gly Ser Ser His Tyr Pro Gly Pro Val Glu
          50           55           60

Gly Arg Phe Thr Ile Ser Arg Asn Tyr Ile Glu Asp Lys Leu Phe Leu
65           70           75           80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
          85           90           95

Thr Lys Tyr Pro Arg Tyr Tyr Asp Met Met Arg Gly Val Arg Asn His
          100          105          110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
          115          120          125

```

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
1           5           10           15

Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His
          20           25           30

Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile
          35           40           45

Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg
50           55           60

Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr Met Glu Leu
65           70           75           80

Arg Ser Leu Arg Ser Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val
          85           90           95

Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp
          100          105          110

Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
          115          120

```

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
1           5           10           15

Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His
          20           25           30

Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile
          35           40           45

Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg
50           55           60

Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala Tyr Met Glu Leu
65           70           75           80

```

Arg Ser Leu Arg Ser Ala Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val  
                             85                            90                            95

Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp  
                             100                            105                            110

Val Trp Gly Lys Gly Thr Lys Val Ile Val Ser Ser  
                             115                            120

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys  
   1                            5                            10                            15

Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His  
                             20                            25                            30

Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile  
                             35                            40                            45

Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg  
                             50                            55                            60

Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala Tyr Met Glu Leu  
   65                            70                            75                            80

Arg Ser Leu Arg Ser Thr Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val  
                             85                            90                            95

Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp  
                             100                            105                            110

Val Trp Gly Lys Gly Thr Lys Val Ile Val Ser Ser  
                             115                            120

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1           5           10           15

Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Ala
          20           25           30

Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Gly Leu Ile
          35           40           45

Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys
          50           55           60

Gly Arg Phe Ser Ile Ser Arg Asn Asn Leu Glu Asp Thr Val Tyr Leu
65           70           75           80

Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala
          85           90           95

Thr Gln Lys Pro Arg Tyr Phe Asp Leu Leu Ser Gly Gln Tyr Arg Arg
          100          105          110

Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val
          115          120          125

Ser Pro
          130

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Ala Gly Gly Ser Leu Arg
1           5           10           15

Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Ala
          20           25           30

```

Trp Val Gly Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Gly Leu Ile  
           35                                  40                                  45  
 Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys  
           50                                  55                                  60  
 Gly Arg Phe Ser Ile Ser Arg Asn Asn Leu Glu Asp Thr Val Tyr Leu  
   65                                  70                                  75                                  80  
 Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
                                   85                                  90                                  95  
 Thr Gln Lys Pro Arg Tyr Phe Asp Leu Leu Ser Gly Gln Tyr Arg Arg  
                                   100                                  105                                  110  
 Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val  
           115                                  120                                  125  
 Ser Pro  
       130

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Leu Glu Glu Ser Gly Gly Gly Leu Ile Lys Pro Gly Gly Ser Leu Arg  
 1                                  5                                  10                                  15  
 Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Thr  
           20                                  25                                  30  
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Leu Ile  
           35                                  40                                  45  
 Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys  
           50                                  55                                  60  
 Gly Arg Phe Thr Ile Ser Arg Asn Asn Leu Glu Asn Thr Val Tyr Leu  
   65                                  70                                  75                                  80  
 Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala  
                                   85                                  90                                  95

Thr Gln Lys Pro Ser Tyr Tyr Asn Leu Leu Ser Gly Gln Tyr Arg Arg  
 100 105 110

Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val  
 115 120 125

Ser Pro

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Glu Glu Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His  
 20 25 30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile  
 35 40 45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
 65 70 75 80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp  
 85 90 95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro  
 100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120 125

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Thr Ser Leu Arg
1           5           10           15

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His
          20           25           30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
          35           40           45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
          50           55           60

Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Glu Met
65           70           75           80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
          85           90           95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
          100          105          110

Asp Tyr Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg
1           5           10           15

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His
          20           25           30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
          35           40           45

```

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60  
 Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
 65 70 75 80  
 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp  
 85 90 95  
 Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro  
 100 105 110  
 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Leu Glu Glu Ser Gly Glu Ala Val Val Gln Pro Gly Thr Ser Leu Arg  
 1 5 10 15  
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His  
 20 25 30  
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile  
 35 40 45  
 Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60  
 Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Glu Met  
 65 70 75 80  
 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp  
 85 90 95  
 Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro  
 100 105 110  
 Asp Tyr Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His  
 20 25 30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile  
 35 40 45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
 65 70 75 80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp  
 85 90 95

Ile Gly Leu Lys Ala Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro  
 100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His  
20 25 30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile  
35 40 45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
50 55 60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met  
65 70 75 80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp  
85 90 95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro  
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120 125

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Leu Glu Gln Ser Gly Gly Gly Val Val Lys Pro Gly Gly Ser Leu Arg  
1 5 10 15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Pro Asn Ala Trp Met Thr  
20 25 30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
35 40 45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Val Phe Leu  
65 70 75 80

Gln Met Asn Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
85 90 95

Thr Arg Tyr Pro Arg Tyr Ser Glu Met Met Gly Gly Val Arg Lys His  
 100 105 110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ser Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Glu Glu Ser Gly Gly Gly Val Val Lys Pro Gly Gly Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Pro Asn Ala Trp Met Thr  
 20 25 30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile  
 35 40 45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Val Phe Leu  
 65 70 75 80

Gln Met Asn Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala  
 85 90 95

Thr Arg Tyr Pro Arg Tyr Ser Glu Met Met Gly Gly Val Arg Lys His  
 100 105 110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ser Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg
1				5					10					15	
Val	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Glu	Met	Asn
			20					25					30		
Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gln	Ile
		35					40					45			
Ser	Ser	Ser	Gly	Ser	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg
		50					55				60				
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Glu	Met
65					70					75				80	
Thr	Ser	Leu	Arg	Val	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly
				85					90					95	
Arg	Arg	Leu	Val	Thr	Phe	Gly	Gly	Val	Val	Ser	Gly	Gly	Asn	Ile	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser						
		115					120								

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu	Glu	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg
1				5					10					15	
Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Asn	Phe	Ser	Asp	Asp	Thr	Met	His
			20					25					30		
Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile
		35					40					45			

Ser Tyr Glu Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60  
 Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr Leu Gln Met  
 65 70 75 80  
 Asp Ser Leu Arg Ala Asp Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asn  
 85 90 95  
 Thr Arg Glu Asn Ile Glu Ala Asp Gly Thr Ala Tyr Tyr Ser Tyr Tyr  
 100 105 110  
 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1 5 10 15  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala  
 20 25 30  
 Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Arg Leu Leu Ile Tyr Ala  
 35 40 45  
 Ala Ser Thr Leu Gln Pro Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 50 55 60  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65 70 75 80  
 Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg Thr Phe  
 85 90 95  
 Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
 1                   5                   10                   15  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala  
                  20                   25                   30  
 Trp Tyr Gln Gln Arg Pro Gly Lys Val Pro Arg Leu Leu Ile Tyr Ala  
                  35                   40                   45  
 Ala Ser Thr Leu Gln Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly  
                  50                   55                   60  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65                   70                   75                   80  
 Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Arg Thr Phe  
                  85                   90                   95  
 Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
                  100                   105

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1                   5                   10                   15  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala  
                  20                   25                   30  
 Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Ala  
                  35                   40                   45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65 70 75 80

Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg Thr Phe  
 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala  
 20 25 30

Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala  
 35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly  
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65 70 75 80

Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro His Thr Phe  
 85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
1                      5                      10                      15  
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ile Ser Asn Tyr Leu  
20                      25                      30  
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
35                      40                      45  
Gly Val Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser  
50                      55                      60  
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
65                      70                      75                      80  
Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Thr Ser Pro Trp Thr  
85                      90                      95  
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
100                      105

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
1                      5                      10                      15  
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asn Tyr Leu  
20                      25                      30  
Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
35                      40                      45  
Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser  
50                      55                      60

Gly Ser Gly Thr Ala Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu  
65 70 75 80

Asp Val Ala Ile Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro Tyr Thr  
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
1 5 10 15

Ala Thr Leu Ser Cys Arg Ala Ser His Arg Val Asn Asn Asn Phe Leu  
20 25 30

Ala Trp Tyr Gln Gln Lys Pro Gln Ala Pro Arg Leu Leu Ile Ser Gly  
35 40 45

Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Asp Asp  
65 70 75 80

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro Leu Tyr Ser  
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Val	Ser	Ala	Ser	Val	Gly	Asp	Thr	1	5	10	15
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	His	Asn	Trp	Leu	Ala	20	25	30	
Trp	Tyr	Gln	Gln	Gln	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	35	40	45	
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Arg	Gly	50	55	60	
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	65	70	75	80
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Ser	Phe	Pro	Lys	Phe	Gly	85	90	95	
Pro	Gly	Thr	Val	Val	Asp	Ile	Lys	Arg	100	105									

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	1	5	10	15
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Ser	Asn	Asn	Tyr	Leu	20	25	30	
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	35	40	45	
Gly	Ser	Ser	Thr	Arg	Gly	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Gly	50	55	60	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	65	70	75	80

Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Asn Ser Val Tyr Thr  
                             85                            90                            95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
                             100                            105

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Gln Ser Pro Asp Thr Leu Ser Leu Asn Pro Gly Glu Arg Ala Thr Leu  
   1                            5                            10                            15

Ser Cys Arg Ala Ser His Arg Ile Ser Ser Lys Arg Leu Ala Trp Tyr  
                             20                            25                            30

Gln His Lys Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr Val Cys Pro  
                             35                            40                            45

Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly  
                             50                            55                            60

Thr Asp Phe Thr Leu Thr Tyr Ser Arg Leu Glu Pro Glu Asp Phe Ala  
   65                            70                            75                            80

Met Tyr Tyr Cys Gln Tyr Tyr Gly Gly Ser Ser Tyr Thr Phe Gly Gln  
                             85                            90                            95

Gly Thr Lys Val Glu Ile Thr Arg  
                             100

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Gln Ser Pro Ser His Leu Ser Leu Ser Pro Gly Glu Arg Ala Ile Leu  
 1                      5                      10                      15  
 Ser Cys Arg Ala Ser Gln Arg Val Ser Ala Pro Tyr Leu Ala Trp Tyr  
                     20                      25                      30  
 Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Gly Ala Ser  
                     35                      40                      45  
 Thr Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly  
                     50                      55                      60  
 Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala  
 65                      70                      75                      80  
 Ile Tyr Tyr Cys Gln Val Tyr Gly Gln Ser Pro Val Leu Phe Gly Gln  
                     85                      90                      95  
 Gly Thr Lys Leu Glu Met Lys Arg  
                     100

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg Ala Thr Leu  
 1                      5                      10                      15  
 Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Ser Phe Leu Ala Trp Tyr  
                     20                      25                      30  
 Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser  
                     35                      40                      45  
 Met Arg Ala Thr Gly Ile Pro Asp Arg Phe Arg Gly Ser Val Ser Gly  
                     50                      55                      60  
 Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala  
 65                      70                      75                      80  
 Val Tyr Tyr Cys Gln Arg Phe Gly Thr Ser Pro Leu Tyr Thr Phe Gly  
                     85                      90                      95

Gln Gly Thr Lys Leu Glu Met Lys Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu  
1 5 10 15  
Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Asn Phe Leu Ala Trp Tyr  
20 25 30  
Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Val His Pro  
35 40 45  
Asn Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly  
50 55 60  
Thr Asp Phe Thr Leu Thr Ile Arg Arg Leu Glu Pro Glu Asp Phe Ala  
65 70 75 80  
Val Tyr Tyr Cys Gln Gln Tyr Gly Ala Ser Leu Val Ser Phe Gly Pro  
85 90 95  
Gly Thr Lys Val His Ile Lys Arg  
100

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
1 5 10 15

Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg Arg Val  
                   20                                  25                                  30

Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His  
                   35                                  40                                  45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser  
                   50                                  55                                  60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu Pro Glu  
                   65                                  70                                  75                                  80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr  
                   85                                  90                                  95

Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg Thr  
                   100                                  105

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Thr Pro Gly Glu Arg  
   1                                  5                                  10                                  15

Ala Thr Leu Ser Cys Arg Thr Ser His Ser Ile Arg Ser Arg Arg Leu  
                   20                                  25                                  30

Ala Trp Tyr Gln Val Lys Gly Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
                   35                                  40                                  45

Gly Val Ser Asn Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser  
                   50                                  55                                  60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
                   65                                  70                                  75                                  80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Arg Tyr Thr  
                   85                                  90                                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr  
                   100                                  105

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Glu Leu Thr Gln Ala Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
 1 5 10 15

Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg Arg Val  
 20 25 30

Arg Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His  
 35 40 45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu Pro Glu  
 65 70 75 80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr  
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Glu Leu Thr Gln Ala Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg  
 1 5 10 15

Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val  
 20 25 30

Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His  
           35                          40                          45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser  
           50                          55                          60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu  
           65                          70                          75                          80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr  
                           85                          90                          95

Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg Thr  
                           100                          105

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
   1                          5                          10                          15

Ala Thr Leu Ser Cys Arg Ala Gly Gln Ser Ile Ser Ser Asn Tyr Leu  
           20                          25                          30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
           35                          40                          45

Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser  
           50                          55                          60

Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Arg Leu Glu Pro Glu  
           65                          70                          75                          80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Ser Pro Tyr Thr  
                           85                          90                          95

Phe Gly Gln Gly Thr Gln Leu Asp Ile Lys Arg Thr  
                           100                          105

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu  
1 5 10 15  
Ser Cys Arg Ala Ser Gln Ser Leu Ser Asn Asn Tyr Leu Ala Trp Tyr  
20 25 30  
Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser  
35 40 45  
Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly  
50 55 60  
Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala  
65 70 75 80  
Val Tyr Tyr Cys Gln Gln Tyr Gly Asn Ser Val Tyr Thr Phe Gly Gln  
85 90 95  
Gly Thr Lys Leu Glu Ile Lys Arg  
100

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1 5 10 15  
 Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Ser Asn Tyr Leu Ala  
 20 25 30  
 Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Gly  
 35 40 45

Ala Ser Thr Leu Gln Ser Gly Gly Pro Ser Arg Phe Ser Gly Ser Gly  
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp  
 65 70 75 80

Val Ala Thr Tyr Ser Cys Gln Asn Tyr Asp Ser Ala Pro Trp Thr Phe  
 85 90 95

Gly Gln Gly Thr Lys Val Asp Ile Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn  
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
 35 40 45

Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Leu Gln Pro Glu Asp  
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Pro Leu Thr  
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Glu	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	1	5	10	15
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Asn	Asn	Tyr	Leu	Asn	20	25	30	
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Ala	Pro	Lys	Leu	Leu	Ile	His	Thr	35	40	45	
Ala	Phe	Asn	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Thr	Ala	50	55	60	
Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Arg	Ser	Leu	Gln	Pro	Glu	Asp	65	70	75	80
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Tyr	Thr	Phe	85	90	95	
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	100	105							

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Glu	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	1	5	10	15
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	20	25	30	
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	35	40	45	
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	50	55	60	

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr  
100 105

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Gln Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr  
100 105

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
 1                      5                      10                      15  
 Thr Cys Arg Ala Ser Gln Thr Ile Ser Ser Tyr Leu Asn Trp Tyr Gln  
                     20                      25                      30  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser  
                     35                      40                      45  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr  
                     50                      55                      60  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 65                      70                      75                      80  
 Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly  
                     85                      90                      95  
 Thr Lys Leu Glu Ile Lys Arg Thr  
                     100

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1                      5                      10                      15  
 Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn  
                     20                      25                      30  
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp  
                     35                      40                      45  
 Ala Ser Asn Ser Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
                     50                      55                      60  
 Ser Gly Arg Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65                      70                      75                      80

Val Ala Thr Tyr Tyr Cys Gln Gln His Gln Asn Val Pro Leu Thr Phe  
                                     85                                    90                                    95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
                                     100                                    105

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
   1                                    5                                    10                                    15

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn His Leu Asn  
                                     20                                    25                                    30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp  
                                     35                                    40                                    45

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
                                     50                                    55                                    60

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp  
   65                                    70                                    75                                    80

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu Thr Phe  
                                     85                                    90                                    95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr  
                                     100                                    105

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 1                      5                      10                      15  
 Ile Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asn Asn Tyr Leu Asn  
                     20                      25                      30  
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly  
                     35                      40                      45  
 Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
                     50                      55                      60  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65                      70                      75                      80  
 Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Asn Thr Pro Pro Trp Thr  
                     85                      90                      95  
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
                     100                      105

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
 1                      5                      10                      15  
 Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Ser Asn Tyr Leu  
                     20                      25                      30  
 Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Val Val Ile Tyr  
                     35                      40                      45  
 Ser Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser  
                     50                      55                      60  
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
 65                      70                      75                      80  
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Asp Ala Gln Tyr Thr  
                     85                      90                      95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Ser Asn  
 1 5 10 15

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Val Val  
 20 25 30

Ile Tyr Ser Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser  
 35 40 45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 50 55 60

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Asp Ala Gln  
 65 70 75 80

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Thr Val Thr  
 1 5 10 15

Phe Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr  
 20 25 30

His Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Asp Ala Ser  
           35                                  40                                  45  
 Asp Leu Glu Ile Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Ala  
           50                                  55                                  60  
 Thr Tyr Phe Ser Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Gly  
   65                                  70                                  75                                  80  
 Thr Tyr Tyr Cys Gln Gln Tyr Ala Asp Leu Ile Thr Phe Gly Gly Gly  
                                   85                                  90                                  95  
 Thr Lys Val Glu Ile Lys Arg Thr  
                                   100

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val  
 1                                  5                                  10                                  15  
 Gly Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg  
                                   20                                  25                                  30  
 Leu Leu Ile Phe Asp Ala Ser Thr Arg Asp Thr Tyr Ile Pro Asp Thr  
                                   35                                  40                                  45  
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ala Leu Thr Ile Ser Ser  
                                   50                                  55                                  60  
 Leu Gln Ser Glu Asp Phe Gly Phe Tyr Tyr Cys Gln Gln Tyr Asp Asn  
   65                                  70                                  75                                  80  
 Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Val Lys Arg Thr  
                                   85                                  90                                  95

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg  
 1                      5                      10                      15

Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val  
                     20                      25                      30

Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His  
                     35                      40                      45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser  
                     50                      55                      60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu  
                     65                      70                      75                      80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr  
                     85                      90                      95

Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg  
                     100                      105

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg  
 1                      5                      10                      15

Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val  
                     20                      25                      30

Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His  
                     35                      40                      45

Gly Val Ser Asn Arg Ala Thr Gly Ile Ser Asp Arg Phe Ser Gly Ser

(2) INFORMATION FOR SEQ ID NO:116:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

(2) INFORMATION FOR SEQ ID NO:117:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Glu Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Asn Ala Gly Glu Arg
1           5           10           15
Ala Thr Leu Ser Cys Arg Ala Ser His Arg Ile Ser Ser Arg Arg Leu
20           25           30
Ala Trp Tyr Gln His Lys Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35           40           45
Gly Val Ser Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
50           55           60
Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Arg Leu Glu Pro Glu
65           70           75           80
Asp Phe Ala Ile Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr
85           90           95
Phe Gly Gln Gly Thr Thr Val Asp Ile Lys Arg
100          105

```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

Glu Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Asn Thr Gly Glu Arg
1           5           10           15
Ala Thr Leu Ser Cys Arg Ala Ser His Arg Ile Gly Ser Arg Arg Leu
20           25           30
Ala Trp Tyr Gln His Arg Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35           40           45
Gly Val Ser Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
50           55           60

```

Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu
65					70					75					80
Asp	Phe	Ala	Ile	Tyr	Tyr	Cys	Gln	Thr	Tyr	Gly	Gly	Ser	Ser	Tyr	Thr
			85						90					95	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg					
		100						105							

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Thr	Pro	Gly	Glu	Arg
1				5					10					15	
Ala	Ile	Leu	Ser	Cys	Lys	Thr	Ser	His	Asn	Ile	Trp	Ser	Arg	Arg	Leu
			20					25					30		
Ala	Trp	Tyr	Gln	Leu	Lys	Ser	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
		35					40					45			
Gly	Val	Ser	Lys	Arg	Ala	Gly	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Pro	Glu
65					70					75					80
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Thr	Tyr	Gly	Gly	Ser	Ala	Tyr	Thr
				85					90					95	
Phe	Gly	Gln	Gly	Thr	Lys	Leu	Asp	Ile	Lys	Arg					
		100						105							

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Thr Pro Gly Glu Arg  
 1                      5                      10                      15  
 Ala Ile Leu Ser Cys Lys Thr Ser His Asn Ile Trp Ser Arg Arg Leu  
                     20                      25                      30  
 Ala Trp Tyr Gln Leu Lys Ser Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
                     35                      40                      45  
 Gly Val Ser Lys Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser  
                     50                      55                      60  
 Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Glu Pro Glu  
 65                      70                      75                      80  
 Asp Phe Ala Val Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ala Tyr Thr  
                     85                      90                      95  
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
                     100                      105

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Ser Thr Pro Gly Glu Arg  
 1                      5                      10                      15  
 Ala Ile Leu Ser Cys Lys Thr Ser His Asn Ile Trp Ser Arg Arg Leu  
                     20                      25                      30  
 Ala Trp Tyr Gln Val Lys Ser Gly Leu Pro Pro Arg Leu Leu Ile His  
                     35                      40                      45  
 Gly Val Ser Arg Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser  
                     50                      55                      60  
 Gly Ser Ala Arg Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Ala  
 65                      70                      75                      80

Asp Phe Ala Val Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Ser  
                                     85                                    90                                    95

Phe Gly Gln Gly Thr Lys Leu Asp Phe Asn Arg  
                                     100                                    105

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Asn Pro Gly Glu Arg  
   1                                    5                                    10                                    15

Ala Val Leu Ser Cys Arg Thr Ser Arg Asn Ile Trp Ser Arg Arg Leu  
                                     20                                    25                                    30

Ala Trp Tyr Gln Val Arg Arg Gly Gln Ala Pro Arg Leu Leu Ile His  
                                     35                                    40                                    45

Gly Val Ser Lys Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser  
                                     50                                    55                                    60

Gly Ser Ala Arg Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
   65                                    70                                    75                                    80

Asp Phe Ala Val Tyr Phe Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr  
                                     85                                    90                                    95

Phe Gly Gln Gly Asn Lys Leu Asp Ile Arg Arg  
                                     100                                    105

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
 1                      5                      10                      15  
 Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
                     20                      25                      30  
 Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp  
                     35                      40                      45  
 Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Pro Pro Lys  
                     50                      55                      60  
 Phe Gln Asp Arg Val Ser Leu Thr Arg Asp Thr Ser Ala Gly Thr Val  
 65                      70                      75                      80  
 Tyr Leu Glu Leu Thr Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
                     85                      90                      95  
 Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
                     100                      105                      110  
 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val  
                     115                      120                      125

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
 1                      5                      10                      15  
 Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
                     20                      25                      30  
 Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp  
                     35                      40                      45  
 Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys  
                     50                      55                      60  
 Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val  
 65                      70                      75                      80

Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
                             85                            90                            95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
                             100                            105                            110

Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Thr Val Thr  
                             115                            120                            125

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
   1                            5                            10                            15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
                             20                            25                            30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp  
                             35                            40                            45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys  
                             50                            55                            60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val  
   65                            70                            75                            80

Tyr Leu Glu Leu Arg Ser Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
                             85                            90                            95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
                             100                            105                            110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val  
                             115                            120

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln	Val	Lys	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Ile	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Arg	Phe	Thr	Asn	20	25	30	
Phe	Val	Leu	His	Trp	Ala	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Pro	Glu	Trp	35	40	45	
Met	Gly	Trp	Phe	Asn	Pro	Ala	Asn	Gly	Ile	Lys	Glu	Ile	Ser	Pro	Lys	50	55	60	
Phe	Gln	Asp	Arg	Val	Ser	Phe	Thr	Gly	Asp	Thr	Ser	Ala	Ser	Thr	Ala	65	70	75	80
Tyr	Val	Glu	Leu	Arg	Asn	Leu	Arg	Ser	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	85	90	95	
Cys	Ala	Arg	Val	Gly	Pro	Trp	Thr	Trp	Asp	Asp	Ser	Pro	Gln	Asp	Asn	100	105	110	
Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	115	120						

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Gln	Val	Lys	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Val	Ser	Cys	Gln	Ala	Ser	Gly	Tyr	Arg	Phe	Ser	Asn	20	25	30	
Phe	Val	Leu	His	Trp	Ala	Arg	Gln	Ala	Pro	Gly	His	Arg	Pro	Glu	Trp	35	40	45	

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys  
 50 55 60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val  
 65 70 75 80

Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Phe Pro Gln Asp Asn  
 100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val  
 115 120

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
 1 5 10 15

Ala Ser Val Lys Leu Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
 20 25 30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp  
 35 40 45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys  
 50 55 60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val  
 65 70 75 80

Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
 100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:129:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Gln	Val	Lys	Leu	Leu	Glu	Gln	Ser	Gly	Thr	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Arg	Phe	Thr	Asn	20	25	30	
Phe	Pro	Leu	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Pro	Glu	Trp	35	40	45	
Met	Gly	Trp	Ile	Lys	Ile	Val	Asn	Gly	Glu	Lys	Lys	Tyr	Ser	Gln	Lys	50	55	60	
Phe	Val	Asp	Arg	Val	Thr	Phe	Thr	Gly	Asp	Thr	Ser	Ala	Asn	Thr	Ala	65	70	75	80
Tyr	Met	Glu	Val	Arg	Gly	Leu	Arg	Ser	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr	85	90	95	
Cys	Ala	Arg	Val	Gly	Glu	Trp	Thr	Trp	Asp	Met	Asp	Pro	Gln	Ala	Asn	100	105	110	
Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	115	120	125				

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gln	Val	Lys	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
20 25 30

Phe Val Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp  
35 40 45

Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys  
50 55 60

Phe Arg Asp Arg Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala  
65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Ile Tyr Tyr  
85 90 95

Cys Ala Arg Val Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn  
100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val  
115 120

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
1 5 10 15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
20 25 30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Thr Gln Asp Leu Glu Trp  
35 40 45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Lys Glu Ile Ser Pro Lys  
50 55 60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val  
65 70 75 80

Tyr Leu Glu Leu Arg Ser Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
                   100                                  105                                  110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val  
           115                                  120

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly  
   1                  5                                  10                                  15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn  
           20                                  25                                  30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp  
       35                                  40                                  45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Pro Pro Lys  
       50                                  55                                  60

Phe Gln Asp Arg Val Ser Leu Thr Arg Asp Thr Ser Ala Gly Thr Val  
       65                                  70                                  75                                  80

Tyr Leu Glu Leu Thr Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr  
                   85                                  90                                  95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn  
                   100                                  105                                  110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val  
       115                                  120

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TCGAGGGTCG GTCGGTCTCT AGACGGTCGG TCGGTCA

37

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTAGTGACCG ACCGACCGTC TAGAGACCGA CCGACCC

37

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CGGTCGGTCG GTCCTCGAGG GTCGGTCGGT CT

32

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTAGAGACCG ACCGACCCTC GAGGACCGAC CGACCGAGCT

40

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAAGGAGACA GGATCCATGA AATAC

25

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

AGGGCGAATT GGATCCCCGGG CCCCC

25

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTAGTCATCA TCATCATCAT TAAGCTAGC

29

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTAGGCTAGC TTAATGATGA TGATGATGA

29

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= J

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 13

(D) OTHER INFORMATION: /label= ZC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ser	Ile	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Gly
1				5					10			

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu	Leu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser
1				5					10					15	

Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Leu	Ser	Ser	Phe	Asp	Trp	Asn
	20							25					30		

Trp	Ile	Arg	Gln	Pro	Ala	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile
	35						40					45			

Tyr	Pro	Ser	Gly	Asn	Thr	His	Tyr	Asn	Pro	Ser	Leu	Arg	Ser	Arg	Val
	50					55					60				

Thr	Met	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Val	Lys	Leu	Thr
65					70					75				80	

Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Arg	Glu	Asn
				85					90					95	

Thr Gly Arg Thr Ile Glu Glu Ile Gly Asn Phe Phe Asp Ile Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:143:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Leu Leu Lys Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg  
 1 5 10 15

Leu Ser Cys Val Ile Ser Ala Phe Ser Phe Ser Gly Tyr Asn Ile Asn  
 20 25 30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile  
 35 40 45

Ser Met Ser Thr Gly Ser Leu Ser Tyr Ala Asp Ser Met Lys Gly Arg  
 50 55 60

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Glu Met  
 65 70 75 80

Ser Ser Leu Thr Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala Arg  
 85 90 95

Thr Pro Leu Val Gly Arg Ala Leu Asp Ile Trp Gly Gln Gly Thr Val  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 115 120

## (2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg  
 1 5 10 15  
 Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met Asn  
 20 25 30  
 Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val Ala Tyr Ile  
 35 40 45  
 Ser Ser Ser Arg Lys Tyr Thr Glu Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60  
 Phe Thr Ile Ser Arg Glu Asn Ala Lys Tyr Ser Val Phe Leu Gln Leu  
 65 70 75 80  
 Asp Ser Leu Thr Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Gly  
 85 90 95  
 Arg Asp Phe Tyr Ser Gly Phe Gly Arg Arg Asp Asp Phe His Leu His  
 100 105 110  
 Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala  
 115 120 125  
 Ser Thr Lys Gly  
 130

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Leu Leu Glu Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu  
 1 5 10 15  
 Arg Ile Ser Cys Val Ala Ser Gly Asp Ile Phe Tyr Ser Tyr Ala Met  
 20 25 30  
 Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ser  
 35 40 45

Ile Ser Gly Thr Gly Gly Ser Asn Tyr Tyr Ala Asp Ser Val Lys Gly  
 50 55 60  
 Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr Leu Gln  
 65 70 75 80  
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg  
 85 90 95  
 Asp Arg Gly Pro Arg Ile Gly Ile Arg Gly Trp Phe Asp Ser Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
 1 5 10 15  
 Leu Ser Cys Ala Ala Ser Gly Phe Leu Tyr Ser Ser Phe Ala Met Ser  
 20 25 30  
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Ala Trp Val Ser Thr Ile  
 35 40 45  
 Ser Ala Ser Gly Gly Ser Thr Lys Tyr Ala Asp Ser Val Lys Gly Arg  
 50 55 60  
 Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Ile Tyr Leu Gln Met  
 65 70 75 80  
 Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asn  
 85 90 95  
 Phe Arg Ala Phe Ala Arg Asp Pro Trp Gly Asp Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser Ala Ser Ala Ser Thr Lys  
 115 120

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Val Ile Val Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Gly  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile His Thr Arg  
 20 25 30

Arg Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val  
 35 40 45  
 Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser  
 85 90 95  
 Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg Thr Val Val  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Gly  
 20 25 30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Ala Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Gly Ser His  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Met Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Gln Gly Ile Gly Arg Phe
      20      25      30
Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
      35      40      45
Tyr Ala Ala Asp Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
      50      55      60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65      70      75      80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
      85      90      95
Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys Arg Thr Val Ala
      100      105      110

```

## (2) INFORMATION FOR SEQ ID NO:151:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Met Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
      20      25      30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Val

```

	35		40		45	
Ile Phe Gly Ala Tyr Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser						
50		55		60		
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu						
65	70		75		80	
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro						
	85		90		95	
Ile Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala						
100		105		110		

## (2) INFORMATION FOR SEQ ID NO:152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..715

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

AGCTTACC ATG GGT GTG CCC ACT CAG GTC CTG GGG TTG CTG CTG CTG TGG	50
Met Gly Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp	
1 5 10	
CTT ACA GAT GCC AGA TGT GAG ATC GTT CTC ACG CAG TCT CCA GGC ACC	98
Leu Thr Asp Ala Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr	
15 20 25 30	
CTG TCT CTG TCT CCA GGG GAA AGA GCC ACC TTC TCC TGT AGG TCC AGT	146
Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser	
35 40 45	
CAC AGC ATT CGC AGC CGC CGC GTA GCC TGG TAC CAG CAC AAA CCT GGC	194
His Ser Ile Arg Ser Arg Arg Val Ala Trp Tyr Gln His Lys Pro Gly	
50 55 60	
CAG GCT CCA AGG CTG GTC ATA CAT GGT GTT TCC AAT AGG GCC TCT GGC	242
Gln Ala Pro Arg Leu Val Ile His Gly Val Ser Asn Arg Ala Ser Gly	
65 70 75	

ATC TCA GAC AGG TTC AGC GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC Ile Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu 80 85 90	290
ACC ATC ACC AGA GTG GAG CCT GAA GAC TTT GCA CTG TAC TAC TGT CAG Thr Ile Thr Arg Val Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln 95 100 105 110	338
GTC TAT GGT GCC TCC TCG TAC ACT TTT GGC CAG GGG ACC AAA CTG GAG Val Tyr Gly Ala Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu 115 120 125	386
AGG AAA CGA ACT GTG CCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT Arg Lys Arg Thr Val Pro Ala Pro Ser Val Phe Ile Phe Pro Pro Ser 130 135 140	434
GAT GAG CAG TTG AAA TCT GGG ACT GCC TCT GTT GTG TGC CTG CTG AAT Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn 145 150 155	482
AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala 160 165 170	530
CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys 175 180 185 190	578
GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp 195 200 205	626
TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu 210 215 220	674
AGT TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TA ATTCTAGAGA Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	725
ATTC	729

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Gly Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr  
 1 5 10 15

Asp Ala Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
 20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser  
 35 40 45

Ile Arg Ser Arg Arg Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ala  
 50 55 60

Pro Arg Leu Val Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser  
 65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
 85 90 95

Thr Arg Val Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr  
 100 105 110

Gly Ala Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys  
 115 120 125

Arg Thr Val Pro Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 15..452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

AATTCGCCGC CACC ATG GAA TGG AGC TGG GTC TTT CTC TTC TTC CTG TCA	50
Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser	
1 5 10	
GTA ACT ACA GGT GTC CAC TCC CAG GTT CAG CTG GTT CAG TCC GGG GCT	98
Val Thr Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala	
15 20 25	
GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCT TGT CAG GCT TCT	146
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Gln Ala Ser	
30 35 40	
GGA TAC AGA TTC AGT AAC TTT GTT ATT CAT TGG GTG CGC CAG GCC CCC	194
Gly Tyr Arg Phe Ser Asn Phe Val Ile His Trp Val Arg Gln Ala Pro	
45 50 55 60	
GGA CAG AGG TTT GAG TGG ATG GGA TGG ATC AAT CCT TAC AAC GGA AAC	242
Gly Gln Arg Phe Glu Trp Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn	
65 70 75	
AAA GAA TTT TCA GCG AAG TTC CAG GAC AGA GTC ACC TTT ACC GCG GAC	290
Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg Val Thr Phe Thr Ala Asp	
80 85 90	
ACA TCC GCG AAC ACA GCC TAC ATG GAG TTG AGG AGC CTC AGG TCT GCA	338
Thr Ser Ala Asn Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala	
95 100 105	
GAC ACG GCT GTT TAT TAT TGT GCG AGA GTG GGG CCA TAT AGT TGG GAT	386
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Gly Pro Tyr Ser Trp Asp	
110 115 120	
GAT TCT CCC CAG GAC AAT TAT TAT ATG GAC GTC TGG GGC AAA GGA ACC	434
Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr	
125 130 135 140	
ACG GTC ATC GTG AGC TCA GCTTCCACCA AGGGCCCATC GGTCTTCCCC	482
Thr Val Ile Val Ser Ser	

145

CTGGCACCCCT	CCTCCAAGAG	CACCTCTGGG	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	542
GACTACTTCC	CCGAACCGGT	GACGGTGTGG	TGGAATCAG	GCGCCCTGAC	CAGCGGCGTG	602
CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	662
GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	722
AACACCAAGG	TGGACAAGAA	AGTTGGTGAG	AGGCCAGCAC	AGGGAGGGAG	GGTGTCTGCT	782
GGAAGCCAGG	CTCAGCGCTC	CTGCCTGGAC	GCATCCCGGC	TATGCAGCCC	CAGTCCAGGG	842
CAGCAAGGCA	GGCCCCGTCT	GCCTCTTCAC	CCGGAGGCCT	CTGCCCCGCC	CACTCATGCT	902
CAGGGAGAGG	GTCTTCTGGC	TTTTTCCCCA	GGCTCTGGGC	AGGCACAGGC	TAGGTGCCCC	962
TAACCCAGGC	CCTGCACACA	AAGGGGCAGG	TGCTGGGCTC	AGACCTGCCA	AGAGCCATAT	1022
CCGGGAGGAC	CCTGCCCCCTG	ACCTAAGCCC	ACCCCAAAGG	CCAAACTCTC	CACTCCCTCA	1082
GCTCGGACAC	CTTCTCTCCT	CCCAGATTGG	AGTAACTCCC	AATCTTCTCT	CTGCAGAGCC	1142
CAAATCTTGT	GACAAAACTC	ACACATGCCC	ACCGTGCCCC	GGTAAGCCAG	CCCAGGCCTC	1202
GCCCTCCAGC	TCAAGGCGGG	ACAGGTGCCC	TAGAGTAGCC	TGCATCCAGG	GACAGGCCCC	1262
AGCCGGGTGC	TGACACGTCC	ACCTCCATCT	CTCCCTCAGC	ACCTGAGGCC	GCGGGAGGAC	1322
CATCAGTCTT	CCTCTTCCCC	CCAAAACCCA	AGGACACCCT	CATGATCTCC	CGGACCCCTG	1382
AGGTCACATG	CGTGGTGGTG	GACGTGAGCC	ACGAAGACCC	TGAGGTCAAG	TTCAACTGGT	1442
ACGTGGACGG	CGTGGAGGTG	CATAATGCCA	AGACAAAGCC	GCGGGAGGAG	CAGTACAACA	1502
GCACGTACCG	TGTGGTCAGC	GTCCTCACCG	TCCTGCACCA	GGACTGGCTG	AATGGCAAGG	1562
AGTACAAGTG	CAAGGTCTCC	AACAAAGCCC	TCCCAGCCCC	CATCGAGAAA	ACCATCTCCA	1622
AAGCCAAAGG	TGGGACCCGT	GGGGTGGGAG	GGCCACATGG	ACAGAGGCCG	GCTCGGCCCC	1682
CCCTCTGCCC	TGAGAGTGAC	CGCTGTACCA	ACCTCTGTCC	CTACAGGGCA	GCCCCGAGAA	1742
CCACAGGTGT	ACACCCTGCC	CCCATCCCGG	GATGAGCTGA	CCAAGAACCA	GGTCAGCCTG	1802
ACCTGCCTGG	TCAAAGGCTT	CTATCCCAGC	GACATCGCCG	TGGAGTGGGA	GAGCAATGGG	1862
CAGCCGGAGA	ACAACTACAA	GACCACGCCT	CCCGTGCTGG	ACTCCGACGG	CTCCTTCTTC	1922
CTCTACAGCA	AGCTCACCGT	GGACAAGAGC	AGGTGGCAGC	AGGGGAACGT	CTTCTCATGC	1982

TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG	2042
GGTAAATGAG TGCGACGGCC GGCAAGCCCC CGCTCCCCGG GCTCTCGCGG TCGCACGAGG	2102
ATGCTTGGA CGTACCCCCT GTACATACTT CCCGGGCGCC CAGCATGGAA ATAAAGCACC	2162
CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT TCCACGGGTC AGGCCGAGTC	2222
TGAGGCCTGA GTGGCATGAG GGAGGCAGAG CGGGTCCCAC TGTCCCCACA CTGGCCCAGG	2282
CTGTGCAGGT GTGCCTGGGC CGCCTAGGGT GGGGCTCAGC CAGGGGCTGC CCTCGGCAGG	2342
GTGGGGGATT TGCCAGCGTT GCCCTCCCTC CAGCAGCACC TGCCCTGGGC TGGGCCACGG	2402
GAAGCCCTAG GAGCCCCTGG GGACAGACAC ACAGCCCCTG CCTCTGTAGG AGACTGTCCT	2462
GTTCTGTGAG CGCCCTGTCC TCCGACCTCC ATGCCCACTC GGGGGCATGC CTAGTCCATG	2522
TGCGTAGGGA CAGGCCCTCC CTCACCCATC TACCCCCAGG GCACTAACCC CTGGCTGTCC	2582
TGCCCAGCCT CGCACCCGCA TGGGGACACA ACCGACTCCG GGGACATGCA CTCTCGGGCC	2642
CTGTGGAGGG ACTGGTGCAG ATGCCACAC ACACACTCAG TCCAGACCCG TTCAACAAAA	2702
CCCCCGCACT GAGGTTGGCC GGCCACACGG CCACCACACA CACACGTGCA CGCCTCACAC	2762
ACGGAGCCTC ACCCGGGCGA ACTGCACAGC ACCCAGACCA GAGCAAGGTC CTCGCACAGG	2822
TGAACACTCC TCGGACACAG GCCCCACGA GCCCCACGG GCACCTCAAG GCCCACGAGC	2882
CTCTCGGCAG CTTCTCCACA TGCTGACCTG CTCAGACAAA CCCAGCCCTC CTCTCACAAG	2942
GGTGCCCCCTG CAGCCGCCAC ACACACACAG GGGATCACAC ACCACGTCAC GTCCCTGGCC	3002
CTGGCCCACT TCCCAGTGCC GCCCTTCCCT GCAGGGCGGA TCATAATCAG CCATACCACA	3062
TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCACACC TCCCCCTGAA CCTGAAACAT	3122
AAAATGAATG CAATTGTTGT TGTAACTTG TTTATTGCAG CTTATAATGG TTACAAATAA	3182
AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTG TAGTTGTGGT	3242
TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTAGATCC	3282

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly  
 1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe  
 35 40 45

Ser Asn Phe Val Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Phe  
 50 55 60

Glu Trp Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser  
 65 70 75 80

Ala Lys Phe Gln Asp Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Val Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln  
 115 120 125

Asp Asn Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val  
 130 135 140

Ser Ser  
 145

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TTCATTGATC ATTAATCAGC CATACCACAT TTGTAGAGGT TTTACTTGCT TTAAAAAACC 60

TCCCACACCT CCCCCTGAAC CTGAAACATA AAATGAATGC AATTGTTGTT GTTAACTTGT 120

TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTT ACAAATAAAG	180
CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG	240
TCTGGATCTC TAGCTTCGTG TCAAGGACGG TGAAGTGCAGT GAATAATAAA ATGTGTGTTT	300
GTCCGAAATA CGCGTTTTGA GATTTCTGTC GCCGACTAAA TTCATGTCGC GCGATAGTGG	360
TGTTTATCGC CGATAGAGAT GGCGATATTG GAAAAATCGA TATTTGAAAA TATGGCATAT	420
TGAAAAATGTC GCCGATGTGA GTTTCTGTGT AACTGATATC GCCATTTTTT CAAAAGTGAT	480
TTTTGGGCAT ACGCGATATC TGGCGATAGC GCTTATATCG TTTACGGGGG ATGGCGATAG	540
ACGACTTTGG TGAAGTGGGC GATTCTGTGT GTCGCAAATA TCGCAGTTTC GATATAGGTG	600
ACAGACGATA TGAGGCTATA TCGCCGATAG AGGCGACATC AAGCTGGCAC ATGGCCAATG	660
CATATCGATC TATACATTGA ATCAATATTG GCCATTAGCC ATATTATTCA TTGGTTATAT	720
AGCATAAATC AATATTGGCT ATTGGCCATT GCATACGTTG TATCCATATC ATAATATGTA	780
CATTTATATT GGCTCATGTC CAACATTACC GCCATGTTGA CATTGATTAT TGAAGTATTA	840
TTAATAGTAA TCAATTACGG GGTCAATTAGT TCATAGCCCA TATATGGAGT TCCGCGTTAC	900
ATAACTTACG GTAAATGGCC CGCCTGGCTG ACCGCCCCAAC GACCCCCGCC CATTGACGTC	960
AATAATGACG TATGTTCCCA TAGTAACGCC AATAGGGACT TTCCATTGAC GTCAATGGGT	1020
GGAGTATTTA CGGTAAACTG CCCACTTGGC AGTACATCAA GTGTATCATA TGCCAAGTAC	1080
GCCCCCTATT GACGTCAATG ACGGTAAATG GCCCGCCTGG CATTATGCCC AGTACATGAC	1140
CTTATGGGAC TTTCTACTT GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT	1200
GATGCGGTTT TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTC	1260
AAGTCTCCAC CCCATTGACG TCAATGGGAG TTTGTTTTGG CACCAAAATC AACGGGACTT	1320
TCCAAAATGT CGTAACAACT CCGCCCCATT GACGCAAATG GGCGGTAGGC GTGTACGGTG	1380
GGAGGTCTAT ATAAGCAGAG CTCGTTTAGT GAACCGTCAG ATCGCCTGGA GACGCCATCC	1440
ACGCTGTTTT GACCTCCATA GAAGACACCG GGACCGATCC AGCCTCCGCG GCCGGGAACG	1500
GTGCATTGGA ACGCGGATTC CCCGTGCCAA GAGTGACGTA AGTACCGCCT ATAGAGTCTA	1560
TAGGCCACCC CCCTTGCTT CTTATGCATG CTATACTGTT TTTGGCTTGG GGTCTATACA	1620
CCCCCGCTTC CTCATGTTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTTATTGA	1680

CCATTATTGA	CCACTCCCCCT	ATTGGTGACG	ATACTTTTCCA	TTACTAATCC	ATAACATGGC	1740
TCTTTGCCAC	AACTCTCTTT	ATTGGCTATA	TGCCAATACA	CTGTCCTTCA	GAGACTGACA	1800
CGGACTCTGT	ATTTTTACAG	GATGGGGTCT	CATTTATTAT	TTACAAATTC	ACATATACAA	1860
CACCACCGTC	CCCAGTGCCC	GCAGTTTTTA	TTAAACATAA	CGTGGGATCT	CCACGCGAAT	1920
CTCGGGTACG	TGTTCCGGAC	ATGGGCTCTT	CTCCGGTAGC	GGCGGAGCTT	CTACATCCGA	1980
GCCCTGCTCC	CATGCCTCCA	GCGACTCATG	GTGCTCGGC	AGCTCCTTGC	TCCTAACAGT	2040
GGAGGCCAGA	CTTAGGCACA	GCACGATGCC	CACCACCACC	AGTGTGCCGC	ACAAGGCCGT	2100
GGCGGTAGGG	TATGTGTCTG	AAAATGAGCT	CGGGGAGCGG	GCTTGCACCG	CTGACGCATT	2160
TGGAAGACTT	AAGGCAGCGG	CAGAAGAAGA	TGCAGGCAGC	TGAGTTGTTG	TGTTCTGATA	2220
AGAGTCAGAG	GTAACCTCCG	TTGCGGTGCT	GTTAACGGTG	GAGGGCAGTG	TAGTCTGAGC	2280
AGTACTCGTT	GCTGCCGCGC	GCGCCACCAG	ACATAATAGC	TGACAGACTA	ACAGACTGTT	2340
CCTTTCCATG	GGTCTTTTCT	GCAGTCACCG	TCCTTGACAC	GAAGCTTGGG	CTGCAGGTCG	2400
ATCGACTCTA	GAGGATCGAT	CCCCGGGGCGA	GCTCGAATTC	GCCGCCACCA	TGGAATGGAG	2460
CTGGGTCTTT	CTCTTCTTCC	TGTCAGTAAC	TACAGGTGTC	CACTCCCAGG	TTCAGCTGGT	2520
TCAGTCCGGG	GCTGAGGTGA	AGAAGCCTGG	GGCCTCAGTG	AAGGTTTCTT	GTCAGGCTTC	2580
TGATACAGA	TTCAGTAACT	TTGTTATTCA	TTGGGTGCGC	CAGGCCCCCG	GACAGAGGTT	2640
TGAGTGGATG	GGATGGATCA	ATCCTTACAA	CGGAAACAAA	GAATTTTCAG	CGAAGTTCCA	2700
GGACAGAGTC	ACCTTTACCG	CGGACACATC	CGCGAACACA	GCCTACATGG	AGTTGAGGAG	2760
CCTCAGGTCT	GCAGACACGG	CTGTTTATTA	TTGTGCGAGA	GTGGGGCCAT	ATAGTTGGGA	2820
TGATTCTCCC	CAGGACAATT	ATTATATGGA	CGTCTGGGGC	AAAGGAACCA	CGGTCATCGT	2880
GAGCTCAGCT	TCCACCAAGG	GCCCATCGGT	CTTCCCCCTG	GCACCCTCCT	CCAAGAGCAC	2940
CTCTGGGGGC	ACAGCGGGCC	TGGGCTGCCT	GGTCAAGGAC	TACTTCCCCG	AACCGGTGAC	3000
GGTGTGCTGG	AACTCAGGCG	CCCTGACCAG	CGGCGTGAC	ACCTTCCCCG	CTGTCCTACA	3060
GTCTCAGGA	CTCTACTCCC	TCAGCAGCGT	GGTGACCGTG	CCCTCCAGCA	GCTTGGGCAC	3120
CCAGACCTAC	ATCTGCAACG	TGAATCACAA	GCCCAGCAAC	ACCAAGGTGG	ACAAGAAAGT	3180
TGGTGAGAGG	CCAGCACAGG	GAGGGAGGGT	GTCTGCTGGA	AGCCAGGCTC	AGCGCTCCTG	3240

CCTGGACGCA	TCCCGGCTAT	GCAGCCCCAG	TCCAGGGCAG	CAAGGCAGGC	CCCGTCTGCC	3300
TCTTCACCCG	GAGGCCTCTG	CCCGCCCCAC	TCATGCTCAG	GGAGAGGGTC	TTCTGGCTTT	3360
TTCCCCAGGC	TCTGGGCAGG	CACAGGCTAG	GTGCCCCATA	CCCAGGCCCT	GCACACAAAG	3420
GGGCAGGTGC	TGGGCTCAGA	CCTGCCAAGA	GCCATATCCG	GGAGGACCCT	GCCCCTGACC	3480
TAAGCCCACC	CCAAAGGCCA	AACTCTCCAC	TCCCTCAGCT	CGGACACCTT	CTCTCCTCCC	3540
AGATTTCGAGT	AACTCCCAAT	CTTCTCTCTG	CAGAGCCCCA	ATCTTGTGAC	AAAACCTACA	3600
CATGCCCACC	GTGCCCAGGT	AAGCCAGCCC	AGGCCTCGCC	CTCCAGCTCA	AGGCGGGACA	3660
GGTGCCCTAG	AGTAGCCTGC	ATCCAGGGAC	AGGCCCCAGC	CGGGTGCTGA	CACGTCCACC	3720
TCCATCTCTC	CCTCAGCACC	TGAGGCCGCG	GGAGGACCAT	CAGTCTTCCT	CTTCCCCCCA	3780
AAACCCAAGG	ACACCCTCAT	GATCTCCCGG	ACCCCTGAGG	TCACATGCGT	GGTGGTGGAC	3840
GTGAGCCACG	AAGACCCTGA	GGTCAAGTTC	AACTGGTACG	TGGACGGCGT	GGAGGTGCAT	3900
AATGCCAAGA	CAAAGCCGCG	GGAGGAGCAG	TACAACAGCA	CGTACCGTGT	GGTCAGCGTC	3960
CTCACCGTCC	TGCACCAGGA	CTGGCTGAAT	GGCAAGGAGT	ACAAGTGCAA	GGTCTCCAAC	4020
AAAGCCCTCC	CAGCCCCCAT	CGAGAAAACC	ATCTCCAAAG	CCAAAGGTGG	GACCCGTGGG	4080
GTGCGAGGGC	CACATGGACA	GAGGCCGGCT	CGGCCCACCC	TCTGCCCTGA	GAGTGACCGC	4140
TGTACCAACC	TCTGTCCCTA	CAGGGCAGCC	CCGAGAACCA	CAGGTGTACA	CCCTGCCCCC	4200
ATCCCGGGAT	GAGCTGACCA	AGAACCAGGT	CAGCCTGACC	TGCCTGGTCA	AAGGCTTCTA	4260
TCCCAGCGAC	ATCGCCGTGG	AGTGGGAGAG	CAATGGGCAG	CCGAGAACA	ACTACAAGAC	4320
CACGCCTCCC	GTGCTGGACT	CCGACGGCTC	CTTCTTCCTC	TACAGCAAGC	TCACCGTGGA	4380
CAAGAGCAGG	TGGCAGCAGG	GGAACGTCTT	CTCATGCTCC	GTGATGCATG	AGGCTCTGCA	4440
CAACCACTAC	ACGCAGAAGA	GCCTCTCCCT	GTCTCCGGGT	AAATGAGTGC	GACGGCCGGC	4500
AAGCCCCCGC	TCCCCGGGCT	CTCGCGGTCT	CACGAGGATG	CTTGGCACGT	ACCCCTGTGA	4560
CATACTTCCC	GGGCGCCCAG	CATGGAAATA	AAGCACCCAG	CGCTGCCCTG	GGCCCTGCG	4620
AGACTGTGAT	GGTTCTTTCC	ACGGGTCAGG	CCGAGTCTGA	GGCCTGAGTG	GCAAGAGGGA	4680
GGCAGAGCGG	GTCCCACTGT	CCCCACACTG	GCCCAGGCTG	TGCAGGTGTG	CCTGGGCCGC	4740
CTAGGGTGGG	GCTCAGCCAG	GGGCTGCCCT	CGGCAGGGTG	GGGGATTTCG	CAGCGTTGCC	4800

CTCCCTCCAG	CAGCACCTGC	CCTGGGCTGG	GCCACGGGAA	GCCCTAGGAG	CCCCTGGGGA	4860
CAGACACACA	CCCCCTGCCT	CTGTAGGAGA	CTGTCCTGTT	CTGTGAGCGC	CCTGTCCTCC	4920
GACCTCCATG	CCCACTCGGG	GGCATGCCTA	GTCCATGTGC	GTAGGGACAG	GCCCTCCCTC	4980
ACCCATCTAC	CCCCACGGCA	CTAACCCCTG	GCTGTCCTGC	CCAGCCTCGC	ACCCGCATGG	5040
GGACACAACC	GA CTCCGGGG	ACATGCACTC	TCGGGCCCTG	TGGAGGGACT	GGTGCAGATG	5100
CCCACACACA	CACTCAGTCC	AGACCCGTTT	AACAAAACCC	CCGCACTGAG	GTTGGCCGGC	5160
CACACGGCCA	CCACACACAC	ACGTGCACGC	CTCACACACG	GAGCCTCACC	CGGGCGAACT	5220
GCACAGCACC	CAGACCAGAG	CAAGGTCCTC	GCACACGTGA	AACTCCTCG	GACACAGGCC	5280
CCCACGAGCC	CCACGCGGCA	CCTCAAGGCC	CACGAGCCTC	TCGGCAGCTT	CTCCACATGC	5340
TGACCTGCTC	AGACAAAACCC	AGCCCTCCTC	TCACAAGGGT	GCCCCTGCAG	CGGCCACACA	5400
CACACAGGGG	ATCACACACC	ACGTACAGTC	CCTGGCCCTG	GCCCACTTCC	CAGTGCCGCC	5460
CTTCCCTGCA	GGGCGGATCA	TAATCAGCCA	TACCACATTT	G TAGAGGTTT	TACTTGCTTT	5520
AAAAAACCTC	CCACACCTCC	CCCTGAACCT	GAAACATAAA	ATGAATGCAA	TTGTTGTTGT	5580
TAACTTGTTT	ATTGCAGCTT	ATAATGGTTA	CAAATAAAGC	AATAGCATCA	CAAATTTTAC	5640
AAATAAAGCA	TTTTTTTAC	TGCATTCTAG	TTGTGGTTTG	TCCAAACTCA	TCAATGTATC	5700
TTATCATGTC	TAGATCCTCT	ACGCCGGACG	CATCGTGGCC	GGCATCACCG	GCGCCACAGG	5760
TGCGGTTGCT	GGCGCCTATA	TCGCCGACAT	CACCGATGGG	GAAGATCGGG	CTCGCCACTT	5820
CGGGCTCATG	AGCGCTTGTT	TCGGCGTGGG	TATGGTGGCA	GGCCCGTGGC	CGGGGGACTG	5880
TTGGGCGCCA	TCTCCTTGCA	TGCACCATTG	CTTGCGGCGG	CGGTGCTCAA	CGGCCTCAAC	5940
CTACTACTGG	GCTGCTTCCT	AATGCAGGAG	TCGCATAAGG	GAGAGCGTCG	ACCTCGGGCC	6000
GCGTTGCTGG	CGTTTTTCCA	TAGGCTCCGC	CCCCCTGACG	AGCATCACAA	AAATCGACGC	6060
TCAAGTCAGA	GGTGGCGAAA	CCCGACAGGA	CTATAAAGAT	ACCAGGCGTT	TCCCCCTGGA	6120
AGCTCCCTCG	TGCGCTCTCC	TGTTCCGACC	CTGCCGCTTA	CCGGATACCT	GTCCGCCTTT	6180
CTCCCTTCGG	GAAGCGTGGC	GCTTTCTCAA	TGCTCACGCT	G TAGGTATCT	CAGTTCGGTG	6240
TAGGTCGTTT	GCTCCAAGCT	GGGCTGTGTG	CACGAACCCC	CCGTTTACGC	CGACCGCTGC	6300
GCCTTATCCG	GTA ACTATCG	TCTTGAGTCC	AACCCGGTAA	GACACGACTT	ATCGCCACTG	6360

GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC	6420
TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG	6480
CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA ACAAACCACC	6540
GCTGGTAGCG GTGGTTTTTT TGTTCGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT	6600
CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAATCACGT	6660
TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTAAATTAA	6720
AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA	6780
TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTTCATC CATAGTTGCC	6840
TGACTCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT TACCATCTGG CCCAGTGCT	6900
GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA	6960
CCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCCTCCAT CCAGTCTATT	7020
AATTGTTGCC GGAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGCG CAACGTTGTT	7080
GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC	7140
GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCATGT TGTGCAAAAA AGCGGTTAGC	7200
TCCTTCGGTC CTCCGATCGT TGTCAGAAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT	7260
ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT	7320
GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGATATG GCGGACCGAG TTGCTCTTGC	7380
CCGGCGTCAA CACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT	7440
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ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT	7560
GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAGG GAATAAGGGC GACACGGAAA	7620
TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT	7680
CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCGCGC	7740
ACATTTCCCC GAAAAGTGCC ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC	7800
TATAAAAATA GCGGTATCAC GAGGCCCTGA TGGCTCTTTG CGGCACCCAT CGTTCGTAAT	7860
GTTCCGTGGC ACCGAGGACA ACCCTCAAGA GAAAATGTAA TCACACTGGC TCACCTTCGG	7920

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GCGGCTTTGG CAGCCAAGCT AGATCCGGCT GTGGAATGTG TGTCAGTTAG GGTGTGGAAA	8040
GTCCCCAGGC TCCCCAGCAG GCAGAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC	8100
CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG	8160
TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC CAGTTCGGCC CATTCTCCGC	8220
CCCATGGCTG ACTAATTTTT TTTATTTATG CAGAGGCCGA GGCCGCTCG GCCTCTGAGC	8280
TATTCCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AACTAGCTTG	8340
GGGCCACCGC TCAGAGCACC TTCCACCATG GCCACCTCAG CAAGTTCCCA CTTGAACAAA	8400
AACATCAAGC AAATGTACTT GTGCCTGCCC CAGGGTGAGA AAGTCCAAGC CATGTATATC	8460
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AAGTGTTAG AAGAGTTACC TGAGTGGAAT TTTGATGGCT CTAGTACCTT TCAGTCTGAG	8580
GGCTCCAACA GTGACATGTA TCTCAGCCCT GTTGCCATGT TTCGGGACCC CTTCCGCAGA	8640
GATCCCAACA AGCTGGTGTT CTGTGAAGTT TTCAAGTACA ACCGGAAGCC TGCAGAGACC	8700
AATTTAAGGC ACTCGTGTA ACGGATAATG GACATGGTGA GCAACCAGCA CCCCTGGTTT	8760
GGAATGGAAC AGGAGTATAC TCTGATGGGA ACAGATGGGC ACCCTTTTGG TTGGCCTTCC	8820
AATGGCTTTC CTGGGCCCCA AGGTCCGTAT TACTGTGGTG TGGGCGCAGA CAAAGCCTAT	8880
GGCAGGGATA TCGTGAGGC TCACTACCGC GCCTGCTTGT ATGCTGGGGT CAAGATTACA	8940
GGAACAAATG CTGAGGTCAT GCCTGCCCAG TGGGAACTCC AAATAGGACC CTGTGAAGGA	9000
ATCCGCATGG GAGATCATCT CTGGGTGGCC CGTTTCATCT TCATCGAGTA TGTGAAGACT	9060
TTGGGGTAAT AGCAACCTTT GACCCCAAGC CCATTCCTGG GAACTGGAAT GGTGCAGGCT	9120
GCCATACCAA CTTTAGCACC AAGGCCATGC GGGAGGAGAA TGGTCTGAAG CACATCGAGG	9180
AGGCCATCGA GAAACTAAGC AAGCGGCACC GGTACCACAT TCGAGCCTAC GATCCCAAGG	9240
GGGGCCTGGA CAATGCCCCG GGTCTGACTG GGTTCACGA AACGTCCAAC ATCAACGACT	9300
TTTCTGCTGG TGTGCGCAAT CGCAGTGCCA GCATCCGCAT TCCCGGACT GTCGGCCAGG	9360
AGAAGAAAGG TTACTTTGAA GACCGCGGCC CCTCTGCCAA TTGTGACCCC TTTGCAGTGA	9420
CAGAAGCCAT CGTCCGCACA TGCCTTCTCA ATGAGACTGG CCAGGAGCCC TTCCAATACA	9480

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AGAGATTTAA AGCTCTAAGG TAAATATAAA ATTTTAAAGT GTATAATGTG TTAAACTACT	9660
GATTCTAATT GTTTGTGTAT TTTAGATTCC AACCTATGGA ACTGATGAAT GGGAGCAGTG	9720
GTGGAATGCC TTTAATGAGG AAAACCTGTT TTGCTCAGAA GAAATGCCAT CTAGTGATGA	9780
TGAGGCTACT GCTGACTCTC AACATTCTAC TCCTCCAAAA AAGAAGAGAA AGGTAGAAGA	9840
CCCCAAGGAC TTTCTTCAG AATTGCTAAG TTTTTTGAGT CATGCTGTGT TTAGTAATAG	9900
AACTCTTGCT TGCTTTGCTA TTTACACCAC AAAGGAAAAA GCTGCACTGC TATACAAGAA	9960
AATTATGGAA AAATATTCTG TAACCTTTAT AAGTAGGCAT AACAGTTATA ATCATAACAT	10020
ACTGTTTTTT CTTACTCCAC ACAGGCATAG AGTGTCTGCT ATTAATAACT ATGCTCAAAA	10080
ATTGTGTACC TTTAGCTTTT TAATTTGTAA AGGGGTTAAT AAGGAATATT TGATGTATAG	10140
TGCCTTGACT AGAGATCATA ATCAGCCATA CCACATTGT AGAGGTTTAA CTTGCTTTAA	10200
AAAACCTCCC ACACCTCCCC CTGAACCTGA AACATAAAAT GAATGCAATT GTTGTGTGTA	10260
ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAAA	10320
ATAAAGCATT TTTTTCAC TG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT	10380
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GTGTTTGTC GAAATACGCG TTTTGAGATT TCTGTCGCCG ACTAAATTCA TGTGCGCGGA	10500
TAGTGGTGTT TATCGCCGAT AGAGATGGCG ATATTGGAAA AATCGATATT TGAAAAATATG	10560
GCATATTGAA AATGTCGCCG ATGTGAGTTT CTGTGTA ACT GATATCGCCA TTTTTC AAA	10620
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CGATAGACGA CTTTGGTGAC TTGGGCGATT CTGTGTGTCG CAAATATCGC AGTTTCGATA	10740
TAGGTGACAG ACGATATGAG GCTATATCGC CGATAGAGGC GACATCAAGC TGGCACATGG	10800
CCAATGCATA TCGATCTATA CATTGAATCA ATATTGGCCA TTAGCCATAT TATTCATTGG	10860
TTATATAGCA TAAATCAATA TTGGCTATTG GCCATTGCAT ACGTTGTATC CATATCATAA	10920
TATGTACATT TATATTGGCT CATGTCCAAC ATTACCGCCA TGTTGACATT GATTATTGAC	10980
TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG	11040

CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC	CCCGCCCATT	11100
GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	11160
ATGGGTGGAG	TATTTACGGT	AAACTGCCCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC	11220
AAGTACGCCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	11280
CATGACCTTA	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	11340
CATGGTGATG	CGGTTTTGGC	AGTACATCAA	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG	11400
ATTTCGAAGT	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	11460
GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT	11520
ACGGTGGGAG	GTCTATATAA	GCAGAGCTCG	TTTAGTGAAC	CGTCAGATCG	CCTGGAGACG	11580
CCATCCACGC	TGTTTTGACC	TCCATAGAAG	ACACCGGGAC	CGATCCAGCC	TCCGCGGCCG	11640
GGAACGGTGC	ATTGGAACGC	GGATTCCCCG	TGCCAAGAGT	GACGTAAGTA	CCGCCTATAG	11700
AGTCTATAGG	CCCACCCCCT	TGGCTTCTTA	TGCATGCTAT	ACTGTTTTTG	GCTTGGGGTC	11760
TATACACCCC	CGCTTCCTCA	TGTTATAGGT	GATGGTATAG	CTTAGCCTAT	AGGTGTGGGT	11820
TATTGACCAT	TATTGACCAC	TCCCCTATTG	GTGACGATAC	TTTCCATTAC	TAATCCATAA	11880
CATGGCTCTT	TGCCACAAC	CTCTTTATTG	GCTATATGCC	AATACACTGT	CCTTCAGAGA	11940
CTGACACGGA	CTCTGTATTT	TTACAGGATG	GGGTCTCATT	TATTATTTAC	AAATTCACAT	12000
ATACAACACC	ACCGTCCCCA	GTGCCCCGAG	TTTTTATTAA	ACATAACGTG	GGATCTCCAC	12060
GCGAATCTCG	GGTACGTGTT	CCGGACATGG	GCTCTTCTCC	GGTAGCGGCG	GAGCTTCTAC	12120
ATCCGAGCCC	TGCTCCCATG	CCTCCAGCGA	CTCATGGTCG	CTCGGCAGCT	CCTTGCTCCT	12180
AACAGTGGAG	GCCAGACTTA	GGCACAGCAC	GATGCCACC	ACCACCAGTG	TGCCGCACAA	12240
GGCCGTGGCG	GTAGGGTATG	TGTCTGAAAA	TGAGCTCGGG	GAGCGGGCTT	GCACCGCTGA	12300
CGCATTGGA	AGACTTAAGG	CAGCGGCAGA	AGAAGATGCA	GGCAGCTGAG	TTGTTGTGTT	12360
CTGATAAGAG	TCAGAGGTAA	CTCCCGTTGC	GGTGCTGTTA	ACGGTGGAGG	GCAGTGTAGT	12420
CTGAGCAGTA	CTCGTTGCTG	CCGCGCGCGC	CACCAGACAT	AATAGCTGAC	AGACTAACAG	12480
ACTGTTCCCT	TCCATGGGTC	TTTTCTGCAG	TCACCGTCCT	TGACACGAAG	CTTACCATGG	12540
GTGTGCCCAC	TCAGGTCCTG	GGGTTGCTGC	TGCTGTGGCT	TACAGATGCC	AGATGTGAGA	12600

TCGTTCTCAC GCAGTCTCCA GGCACCCTGT CTCTGTCTCC AGGGGAAAGA GCCACCTTCT	12660
CCTGTAGGTC CAGTCACAGC ATTCGCAGCC GCCGCGTAGC CTGGTACCAG CACAAACCTG	12720
GCCAGGCTCC AAGGCTGGTC ATACATGGTG TTTCCAATAG GGCCTCTGGC ATCTCAGACA	12780
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GGACCAAACCT GGAGAGGAAA CGAACTGTGC CTGCACCATC TGTCTTCATC TTCCCGCCAT	12960
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CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG	13080
AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC	13140
TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC	13200
TGAGATCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TTAATTCTAG AGAA	13254

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CAGGTTTCAGC TGGTTCAGTC CGGGGCT

27

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCTTGAGCT CACGATGACC GTGGTTCCTT GGCCCCGAGAC GTCC

44

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGCCGCGAAT TCGCCGCCAC CATGGAATGG AGCTGGGTCT TTCTCTTCTT CCTGTCAGTA

60

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AGCCCCGGAC TGAACCAGCT GAACCTG

27

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGAGTTGAGG AGCCTCAGGT CTGCAGACAC GG

32

(2) INFORMATION FOR SEQ ID NO:162:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CCGTGTCTGC AGACCTGTGG CTCCTCAACT CC

32

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATGCCAGAT GTGAGATCGT TCTCACGCAG TCT

33

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GCGGGATCCG AATTCTCTAG AATTAACACT CTCCCCTGTT GAAGCTCTTT GTGACGGGCG

60

AACTCAG

67

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCGCGAATTC ACCATGGGTG TGCCCACTCA GGTCTGGGG GTTGCTGCTG C

51

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AGACTGCGTG AGAACGATCT CACATCTGGC ATC

33

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GCGCAAGCTT ACCATGGGTG TGCCCACTCA GGTCTGGGG TTGCTGCTGC

50

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 729 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCTCTA GAATTAACAC TCTCCCCTGT TGAAGCTCTT TGTGACGGGC GAACTCAGGC	60
CCTGATGGGT GACTTCGCAG GCGTAGACTT TGTGTTTCTC GTAGTCTGCT TTGCTCAGCG	120
TCAGGGTGCT GCTGAGGCTG TAGGTGCTGT CCTTGCTGTC CTGCTCTGTG AACTCTCCT	180
GGGAGTTACC CGATTGGAGG GCGTTATCCA CCTTCCACTG TACTTTGGCC TCTCTGGGAT	240
AGAAGTTATT CAGCAGGCAC ACAACAGAGG CAGTCCCAGA TTTCAACTGC TCATCAGATG	300
GCGGGAAGAT GAAGACAGAT GGTGCAGGCA CAGTTCGTTT CCTCTCCAGT TTGGTCCCCT	360
GGCCAAAAGT GTACGAGGAG GCACCATAGA CCTGACAGTA GTACAGTGCA AAGTCTTCAG	420
GCTCCACTCT GGTGATGGTG AGAGTGAAGT CTGTCCCAGA CCCACTGCCG CTGAACCTGT	480
CTGAGATGCC AGAGGCCCTA TTGGAACAC CATGTATGAC CAGCCTTGA GCCTGGCCAG	540
GTTTGTGCTG GTACCAGGCT ACGCGGCGGC TGCGAATGCT GTGACTGGAC CTACAGGAGA	600
AGGTGGCTCT TCCCCCTGGA GACAGAGACA GGTGCCTGG AGACTGCGTG AGAACGATCT	660
CACATCTGGC ATCTGTAAGC CACAGCAGCA GCAACCCAG GACCTGAGTG GGCACACCCA	720
TGGTAAGCT	729

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGATCTAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAATA GAATGCAGTG	60
AAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG	120
CTGCAATAAA CAAGTTAACA ACAACAATTG CATTCATTTT ATGTTTCAGG TTCAGGGGGA	180

GGTGTGGGAG	GTTTTTTTAAA	GCAAGTAAAA	CCTCTACAAA	TGTGGTATGG	CTGATTATGA	240
TCCGCCCTGC	AGGGAAGGGC	GGCACTGGGA	AGTGGGCCAG	GGCCAGGGAC	GTGACGTGGT	300
GTGTGATCCC	CTGTGTGTGT	GTGGCGGCTG	CAGGGGCACC	CTTGTGAGAG	GAGGGCTGGG	360
TTTGTCTGAG	CAGGTCAGCA	TGTGGAGAAG	CTGCCGAGAG	GCTCGTGGGC	CTTGAGGTGC	420
CGCGTGGGGC	TCGTGGGGGC	CTGTGTCCGA	GGAGTGTTCA	CGTGTGCGAG	GACCTTGCTC	480
TGGTCTGGGT	GCTGTGCAGT	TCGCCCCGGT	GAGGCTCCGT	GTGTGAGGCG	TGCACGTGTG	540
TGTGTGGTGG	CCGTGTGGCC	GGCCAACCTC	AGTGCGGGGG	TTTTGTTGAA	CGGGTCTGGA	600
CTGAGTGTGT	GTGTGGGCAT	CTGCACCAGT	CCCTCCACAG	GGCCCGAGAG	TGCATGTCCC	660
CGGAGTCGGT	TGTGTCCCCA	TGCGGGTGCG	AGGCTGGGCA	GGACAGCCAG	GGGTTAGTGC	720
CGTGGGGGTA	GATGGGTGAG	GGAGGGCCTG	TCCCTACGCA	CATGGACTAG	GCATGCCCCC	780
GAGTGGGCAT	GGAGGTCGGA	GGACAGGGCG	CTCACAGAAC	AGGACAGTCT	CCTACAGAGG	840
CAGGGGCTGT	GTGTCTGTCC	CCAGGGGCTC	CTAGGGCTTC	CCGTGGCCCA	GCCCAGGGCA	900
GGTGCTGCTG	GAGGGAGGGC	AACGCTGGCA	AATCCCCCAC	CCTGCCGAGG	GCAGCCCCTG	960
GCTGAGCCCC	ACCCTAGGCG	GCCCAGGCAC	ACCTGCACAG	CCTGGGCCAG	TGTGGGGACA	1020
GTGGGACCCG	CTCTGCCTCC	CTCATGCCAC	TCAGGCCTCA	GACTCGGCCT	GACCCGTGGA	1080
AAGAACCATC	ACAGTCTCGC	AGGGGCCCAG	GGCAGCGCTG	GGTGCTTTAT	TTCCATGCTG	1140
GGCGCCCGGG	AAGTATGTAC	AGGGGGTACG	TGCCAAGCAT	CCTCGTGCGA	CCGCGAGAGC	1200
CCGGGGAGCG	GGGGCTTGCC	GGCCGTGCGA	CTCATTTACC	CGGAGACAGG	GAGAGGCTCT	1260
TCTGCGTGTA	GTGGTTGTGC	AGAGCCTCAT	GCATCACGGA	GCATGAGAAG	ACGTTCCCCT	1320
GCTGCCACCT	GCTCTTGTC	ACGGTGAGCT	TGCTGTAGAG	GAAGAAGGAG	CCGTGCGAGT	1380
CCAGCACGGG	AGGCGTGGTC	TTGTAGTTGT	TCTCCGGCTG	CCCATTGCTC	TCCCACTCCA	1440
CGGCGATGTC	GCTGGGATAG	AAGCCTTTGA	CCAGGCAGGT	CAGGCTGACC	TGGTTCTTGG	1500
TCAGCTCATC	CCGGGATGGG	GGCAGGGTGT	ACACCTGTGG	TTCTCGGGGC	TGCCCTGTAG	1560
GGACAGAGGT	TGGTACAGCG	GTCACCTCTCA	GGGCAGAGGG	TGGGCCGAGC	GGGCCTCTGT	1620
CCATGTGGCC	CTCGCACCCC	ACGGGTCCCA	CCTTTGGCTT	TGGAGATGGT	TTTCTCGATG	1680
GGGGCTGGGA	GGGCTTTGTT	GGAGACCTTG	CACTTGTA	CACTTGTA	CACTTGTA	1740

TGGTGCAGGA CGGTGAGGAC GCTGACCACA CGGTACGTGC TGTGTACTG CTCCTCCCGC	1800
GGCTTTGTCT TGGCATTATG CACCTCCAGC CCGTCCACGT ACCAGTTGAA CTTGACCTCA	1860
GGGTCTTCGT GGCTCACGTC CACCACCAGC CATGTGACCT CAGGGGTCCG GGAGATCATG	1920
AGGGTGTCTT TGGGTTTTGG GGGGAAGAGG AAGACTGATG GTCCTCCCGC GGCCTCAGGT	1980
GCTGAGGGAG AGATGGAGGT GGACGTGTCA GCACCCGGCT GGGGCCTGTC CCTGGATGCA	2040
GGCTACTCTA GGGCACCTGT CCCGCCTTGA GCTGGAGGGC GAGGCCTGGG CTGGCTTACC	2100
TGGGCACGGT GGGCATGTGT GAGTTTTGTC ACAAGATTG GGCTCTGCAG AGAGAAGATT	2160
GGGAGTTACT CGAATCTGGG AGGAGAGAAG GTGTCCGAGC TGAGGGAGTG GAGAGTTTGG	2220
CCTTTGGGGT GGGCTTAGGT CAGGGGCAGG GTCCTCCCGG ATATGGCTCT TGGCAGGTCT	2280
GAGCCCAGCA CCTGCCCCCTT TGTGTGCAGG GCCTGGGTGA GGGGCACCTA GCCTGTGCCT	2340
GCCCAGAGCC TGGGGAAGAA GCCAGAAGAC CCTCTCCCTG AGCATGAGTG GGGCGGGCAG	2400
AGGCCTCCGG GTGAAGAGGC AGACGGGGCC TGCCTTGCTG CCCTGGACTG GGGCTGCATA	2460
GCCGGGATGC GTCCAGGCAG GAGCGCTGAG CCTGGCTTCC AGCAGACACC CTCCCTCCCT	2520
GTGCTGGCCT CTCACCAACT TTCTTGTCCA CCTTGGTGTT GCTGGGCTTG TGATTACGT	2580
TGCAGATGTA GGTCTGGGTG CCCAAGCTGC TGGAGGGCAC GGTACCACG CTGCTGAGGG	2640
AGTAGAGTCC TGAGGACTGT AGGACAGCCG GGAAGGTGTG CACGCCGCTG GTCAGGGCGC	2700
CTGAGTTCCA CGACACCGTC ACCGGTTCCG GGAAGTAGTC CTTGACCAGG CAGCCCAGGG	2760
CCGCTGTGCC CCCAGAGGTG CTCTTGGAGG AGGGTGCCAG GGGGAAGACC GATGGGCCCT	2820
TGGTGGAAGC TGAGCTCACG ATGACCGTGG TTCCTTTGCC CCAGACGTCC ATATAATAAT	2880
TGTCCTGGGG AGAATCATCC CAACTATATG GCCCCACTCT CGCACAATAA TAAACAGCCG	2940
TGTCTGCAGA CCTGAGGCTC CTCAACTCCA TGTAGGCTGT GTTCGCGGAT GTGTCCGCGG	3000
TAAAGGTGAC TCTGTCTGG AACTTCGCTG AAAATTCTTT GTTTCGGTTG TAAGGATTGA	3060
TCCATCCCAT CCACTCAAAC CTCTGTCCGG GGGCCTGGCG CACCCAATGA ATAACAAAGT	3120
TACTGAATCT GTATCCAGAA GCCTGACAAG AAACCTTCAC TGAGGCCCCA GGCTTCTTCA	3180
CCTCAGCCCC GGAAGTGAACC AGCTGAACCT GGGAGTGGAC ACCTGTAGTT ACTGACAGGA	3240
AGAAGAGAAA GACCCAGCTC CATTCCATGG TGGCGGCGAA TT	3282

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TTCTCTAGAA TTAACACTCT CCCCTGTTGA AGCTCTTTGT GACGGGCGAT CTCAGGCCCT	60
GATGGGTGAC TTCGCAGGCG TAGACTTTGT GTTTCTCGTA GTCTGCTTTG CTCAGCGTCA	120
GGGTGCTGCT GAGGCTGTAG GTGCTGTCCT TGCTGTCCTG CTCTGTGACA CTCTCCTGGG	180
AGTTACCCGA TTGGAGGGCG TTATCCACCT TCCACTGTAC TTTGGCCTCT CTGGGATAGA	240
AGTTATTAG CAGGCACACA ACAGAGGCAG TCCCAGATTT CAACTGCTCA TCAGATGGCG	300
GGAAGATGAA GACAGATGGT GCAGGCACAG TTCGTTTCCT CTCCAGTTTG GTCCCCTGGC	360
CAAAAGTGTA CGAGGAGGCA CCATAGACCT GACAGTAGTA CAGTGCAAAG TCTTCAGGCT	420
CCACTCTGGT GATGGTGAGA GTGAAGTCTG TCCCAGACCC ACTGCCGCTG AACCTGTCTG	480
AGATGCCAGA GGCCCTATTG GAAACACCAT GTATGACCAG CCTTGGAGCC TGGCCAGGTT	540
TGTGCTGGTA CCAGGCTACG CGGCGGCTGC GAATGCTGTG ACTGGACCTA CAGGAGAAGG	600
TGGCTCTTTC CCCTGGAGAC AGAGACAGGG TGCCTGGAGA CTGCGTGAGA ACGATCTCAC	660
ATCTGGCATC TGTAAGCCAC AGCAGCAGCA ACCCCAGGAC CTGAGTGGGC ACACCCATGG	720
TAAGCTTCGT GTCAAGGACG GTGACTGCAG AAAAGACCCA TGGAAAGGAA CAGTCTGTTA	780
GTCTGTCAGC TATTATGTCT GGTGGCGCGC GCGGCAGCAA CGAGTACTGC TCAGACTACA	840
CTGCCCTCCA CCGTTAACAG CACCGCAACG GGAGTTACCT CTGACTCTTA TCAGAACACA	900
ACAACTCAGC TGCCTGCATC TTCTTCTGCC GCTGCCTTAA GTCTTCCAAA TGGGTCAGCG	960
GTGCAAGCCC GCTCCCCGAG CTCATTTTCA GACACATACC CTACCGCCAC GGCCTTGTGC	1020
GGCACACTGG TGGTGGTGGG CATCGTGCTG TGCCTAAGTC TGGCCTCCAC TGTTAGGAGC	1080
AAGGAGCTGC CGAGCGACCA TGAGTCGCTG GAGGCATGGG AGCAGGGCTC GGATGTAGAA	1140

GCTCCGCCGC TACCGGAGAA GAGCCCATGT CCGGAACACG TACCCGAGAT TCGCGTGGAG	1200
ATCCACAGTT ATGTTTAATA AAAACTGCGG GCACTGGGGA CGGTGGTGTT GTATATGTGA	1260
ATTTGTAAAT AATAAATGAG ACCCCATCCT GTAAAAATAC AGAGTCCGTG TCAGTCTCTG	1320
AAGGACAGTG TATTGGCATA TAGCCAATAA AGAGAGTTGT GGCAAAGAGC CATGTTATGG	1380
ATTAGTAATG GAAAGTATCG TCACCAATAG GGGAGTGGTC AATAATGGTC AATAACCCAC	1440
ACCTATAGGC TAAGCTATAC CATCACCTAT AACATGAGGA AGCGGGGGTG TATAGACCCC	1500
AAGCCAAAAA CAGTATAGCA TGCATAAGAA GCCAAGGGGG TGGGCCTATA GACTCTATAG	1560
GCGGTACTTA CGTCACTCTT GGCACGGGGA ATCCGCGTTC CAATGCACCG TTCCCGGCCG	1620
CGGAGGCTGG ATCGGTCCCG GTGTCTTCTA TGGAGGTCAA AACAGCGTGG ATGGCGTCTC	1680
CAGGCGATCT GACGGTTCAC TAAACGAGCT CTGCTTATAT AGACCTCCCA CCGTACACGC	1740
CTACCGCCCA TTTGCGTCAA TGGGGCGGAG TTGTTACGAC ATTTTGAAA GTCCCGTTGA	1800
TTTTGGTGCC AAAACAACT CCCATTGACG TCAATGGGGT GGAGACTTGG AAATCCCCGT	1860
GAGTCAAACC GCTATCCACG CCCATTGATG TACTGCCAAA ACCGCATCAC CATGGTAATA	1920
GCGATGACTA ATACGTAGAT GTACTGCCAA GTAGGAAAGT CCCATAAGGT CATGTACTGG	1980
GCATAATGCC AGGCGGGCCA TTTACCGTCA TTGACGTCAA TAGGGGGCGT ACTTGGCATA	2040
TGATACACTT GATGTACTGC CAAGTGGGCA GTTTACCGTA AATACTCCAC CCATTGACGT	2100
CAATGGAAAG TCCCTATTGG CGTTACTATG GGAACATACG TCATTATTGA CGTCAATGGG	2160
CGGGGGTCGT TGGGCGGTCA GCCAGGCGGG CCATTTACCG TAAGTTATGT AACGCGGAAC	2220
TCCATATATG GGCTATGAAC TAATGACCCC GTAATTGATT ACTATTAATA ACTAGTCAAT	2280
AATCAATGTC AACATGGCGG TAATGTTGGA CATGAGCCAA TATAAATGTA CATATTATGA	2340
TATGGATACA ACGTATGCAA TGGCCAATAG CCAATATTGA TTTATGCTAT ATAACCAATG	2400
AATAATATGG CTAATGGCCA ATATTGATT C AATGTATAGA TCGATATGCA TTGGCCATGT	2460
GCCAGCTTGA TGTGCGCTCT ATCGGCGATA TAGCCTCATA TCGTCTGTCA CCTATATCGA	2520
AACTGCGATA TTTGCGACAC ACAGAATCGC CCAAGTCACC AAAGTCGTCT ATCGCCATCC	2580
CCCGTAAACG ATATAAGCGC TATCGCCAGA TATCGCGTAT GCCCAAAAAT CACTTTTGGG	2640
AAAATGGCGA TATCAGTTAC ACAGAACTC ACATCGGCGA CATTTTCAAT ATGCCATATT	2700

TTCAAATATC GATTTTTTCCA ATATCGCCAT CTCTATCGGC GATAAACACC ACTATCGCGC	2760
GACATGAATT TAGTCGGCGA CAGAAATCTC AAAACGCGTA TTTGGGACAA ACACACATT	2820
TATTATTAC TGCAGTCACC GTCCTTGACA CGAAGCTAGA GATCCAGACA TGATAAGATA	2880
CATTGATGAG TTTGGACAAA CCACAACACTAG AATGCAGTGA AAAAAATGCT TTATTTGTGA	2940
AATTTGTGAT GCTATTGCTT TATTTGTAAC CATTATAAGC TGCAATAAAC AAGTTAACAA	3000
CAACAATTGC ATTCATTTTA TGTTTCAGGT TCAGGGGGAG GTGTGGGAGG TTTTTTAAAG	3060
CAAGTAAAC CTCTACAAAT GTGGTATGGC TGATTATGAT CTCTAGTCAA GGCACATAC	3120
ATCAAATATT CCTTATTAAC CCCTTTACAA ATTAAAAAGC TAAAGGTACA CAATTTTTGA	3180
GCATAGTTAT TAATAGCAGA CACTCTATGC CTGTGTGGAG TAAGAAAAAA CAGTATGTTA	3240
TGATTATAAC TGTTATGCCT ACTTATAAAG GTTACAGAAT ATTTTCCAT AATTTCTTG	3300
TATAGCAGTG CAGCTTTTTT CTTTGTGGTG TAAATAGCAA AGCAAGCAAG AGTTCTATTA	3360
CTAAACACAG CATGACTCAA AAAACTTAGC AATTCTGAAG GAAAGTCCTT GGGGTCTTCT	3420
ACCTTTCTCT TCTTTTTTGG AGGAGTAGAA TGTTGAGAGT CAGCAGTAGC CTCATCATCA	3480
CTAGATGGCA TTTCTTCTGA GCAAAACAGG TTTTCCTCAT TAAAGGCATT CCACCACTGC	3540
TCCCATTAT CAGTTCCATA GGTGGAATC TAAAATACAC AAACAATTAG AATCAGTAGT	3600
TTAACACATT ATACACTTAA AAATTTTATA TTTACCTTAG AGCTTTAAAT CTCTGTAGGT	3660
AGTTTGTCCA ATTATGTCAC ACCACAGAAG TAAGGTTTCT TCACAAAGAT CTCTCTGGGG	3720
CGGGGTGGGA TGAAC TAGGA AAGGCTCAAG ATCACTCAA GTCTAATTAG TTTTGTATT	3780
GGAAGGGCTC GTGGCCAGTC TCATTGAGAA GGCATGTGCG GACGATGGCT TCTGTCACTG	3840
CAAAGGGGTC ACAATTGGCA GAGGGGCCGC GGTCTTCAA GTAACCTTTC TTCTCCTGGC	3900
CGACAGTCCG GGAATGCGG ATGCTGGCAC TGCGATTGGC GACACCAGCA GAAAAGTCGT	3960
TGATGTTGGA CGTTTCGTGG AACCAGTCA GACCACGGGC ATTGTCCAGG CCCCCCTTGG	4020
GATCGTAGGC TCGAATGTGG TACCGGTGCC GCTTGCTTAG TTTCTCGATG GCCTCCTCGA	4080
TGTGCTTACG ACCATTCTCC TCCCGCATGG CCTTGGTGCT AAAGTTGGTA TGGCAGCCTG	4140
CACCATTCCA GTTCCCAGGA ATGGGCTTGG GGTCAAAGGT TGCTATTACC CCAAAGTCTT	4200
CACATACTCG ATGAAGATGA AACGGGCCAC CCAGAGATGA TCTCCCATGC GGATTCCTTC	4260

ACAGGGTCCT ATTTGGAGTT CCCACTGGGC AGGCATGACC TCAGCATTG TTCCTGTAAT	4320
CTTGACCCCA GCATACAAGC AGGCGCGGTA GTGAGCCTCC ACGATATCCC TGCCATAGGC	4380
TTTGTCTGCG CCCACACCAC AGTAATACGG ACCTTGGGGC CCAGGAAAGC CATTGGAAGG	4440
CCAACCAAAA GGGTGCCCAT CTGTTCCCAT CAGAGTATAC TCCTGTTCCA TTCCAAACCA	4500
GGGGTGCTGG TTGCTCACCA TGTCCATTAT CCGTTTACAC GAGTGCCTTA AATTGGTCTC	4560
TGCAGGCTTC CGGTTGTACT TGAAAATTTC ACAGAACACC AGCTTGTTGG GATCTCTGCG	4620
GAAGGGGTCC CGAAACATGG CAACAGGGCT GAGATACATG TCACTGTTGG AGCCCTCAGA	4680
CTGAAAGGTA CTAGAGCCAT CAAAATTCCA CTCAGGTAAC TCTTCTACAC ACTTGGGCTC	4740
ACAGTCCAGG GTGCGGGTTT TGCAGCGCAG TCCTTCTCCA GTACCATCAA CCCAGATATA	4800
CATGGCTTGG ACTTTCTCAC CCTGGGGCAG GCACAAGTAC ATTTGCTTGA TGTTTTTGT	4860
CAAGTGGGAA CTGCTGAGG TGGCCATGGT GGAAGGTGCT CTGAGCGGTG GCCCCAAGCT	4920
AGTTTTTGCA AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG	4980
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGGGGCGGAG	5040
AATGGGCGGA ACTGGGCGGA GTTAGGGGCG GGATGGGCGG AGTTAGGGGC GGGACTATGG	5100
TTGCTGACTA ATTGAGATGC ATGCTTTGCA TACTTCTGCC TGCTGGGGAG CCTGGTTGCT	5160
GACTAATTGA GATGCATGCT TTGCATACTT CTGCCTGCTG GGGAGCCTGG GGACTTTCCA	5220
CACCCTAACT GACACACATT CCACAGCCGG ATCTAGCTTG GCTGCCAAAG CCGCAAGGAA	5280
TTTACCAACC TTCTTAAACA TAAAGTGTCT CTTATAAAC GCAGAAAGGC CCACCCGAAG	5340
GTGAGCCAGT GTGATTACAT TTTCTCTTGA GGGTTGTCCT CGGTGCCACG GAACATTACG	5400
AACGATGGGT GCCGCAAAGA GCCATCAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA	5460
TGTCATGATA ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCCGGGAA ATGTGCGCGG	5520
AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA	5580
ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG	5640
TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC	5700
GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT	5760
GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	5820

GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG CCGGGCAAGA	5880
GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC	5940
AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT	6000
GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC	6060
CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	6120
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC	6180
GTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA	6240
CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG	6300
GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGTCT CTGGGTATCA TTGCAGCACT	6360
GGGGCCAGAT GGTAAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC	6420
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA	6480
ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT TTAAAACTTC ATTTTAAATT	6540
TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA	6600
GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC	6660
TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT	6720
TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT TCAGCAGAGC	6780
GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC	6840
TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTGA CCAGTGGCTG CTGCCAGTGG	6900
CGATAAGTCG TGTCTTACCG GGTGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG	6960
GTCGGGCTGA ACGGGGGGTT CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA	7020
ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC	7080
GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG	7140
GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG	7200
ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCCCG	7260
AGGTCGACGC TCTCCCTTAT GCGACTCCTG CATTAGGAAG CAGCCCAGTA GTAGGTTGAG	7320
GCCGTTGAGC ACCGCCGCCG CAAGGAATGG TGCATGCAAG GAGATGGCGC CCAACAGTCC	7380

CCCCGGCCACG GGCCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG	7440
CGAGCCCGAT CTTCCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG	7500
GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCTAGACATG ATAAGATACA	7560
TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA AAAATGCTTT ATTTGTGAAA	7620
TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTAACAACA	7680
ACAATTGCAT TCATTTTATG TTTCAGGTTT AGGGGGAGGT GTGGGAGGTT TTTTAAAGCA	7740
AGTAAAACCT CTACAAATGT GGTATGGCTG ATTATGATCC GCCCTGCAGG GAAGGGCGGC	7800
ACTGGGAAGT GGGCCAGGGC CAGGGACGTG ACGTGGTGTG TGATCCCCTG TGTGTGTGTG	7860
GCGGCTGCAG GGGCACCCTT GTGAGAGGAG GGCTGGGTTT GTCTGAGCAG GTCAGCATGT	7920
GGAGAAGCTG CCGAGAGGCT CGTGGGCCTT GAGGTGCCGC GTGGGGCTCG TGGGGGCCTG	7980
TGTCCGAGGA GTGTTACGT GTGCGAGGAC CTTGCTCTGG TCTGGGTGCT GTGCAGTTCTG	8040
CCCCGGTGAG GCTCCGTGTG TGAGGCGTGC ACGTGTGTGT GTGGTGCCG TGTGGCCGGC	8100
CAACCTCAGT GCGGGGGTTT TGTGAACGG GTCTGGACTG AGTGTGTGTG TGGGCATCTG	8160
CACCAGTCCC TCCACAGGGC CCGAGAGTGC ATGTCCCCGG AGTCGGTTGT GTCCCCATGC	8220
GGGTGCGAGG CTGGGCAGGA CAGCCAGGGG TTAGTGCCGT GGGGGTAGAT GGGTGAGGGA	8280
GGGCCTGTCC CTACGCACAT GGA CTAGGCA TGCCCCCGAG TGGGCATGGA GGTCGGAGGA	8340
CAGGGCGCTC ACAGAACAGG ACAGTCTCCT ACAGAGGCAG GGGCTGTGTG TCTGTCCCCA	8400
GGGGCTCCTA GGGCTTCCCG TGGCCCAGCC CAGGGCAGGT GCTGCTGGAG GGAGGGCAAC	8460
GCTGGCAAAT CCCCCACCCT GCCGAGGGCA GCCCCTGGCT GAGCCCCACC CTAGGCGGCC	8520
CAGGCACACC TGCACAGCCT GGGCCAGTGT GGGGACAGTG GGACCCGCTC TGCCTCCCTC	8580
ATGCCACTCA GGCCTCAGAC TCGGCCTGAC CCGTGGAAG AACCATCACA GTCTCGCAGG	8640
GGCCAGGGC AGCGCTGGGT GCTTTATTTC CATGCTGGGC GCCCGGAAG TATGTACAGG	8700
GGGTACGTGC CAAGCATCCT CGTGCGACCG CGAGAGCCCG GGGAGCGGGG GCTTGCCGGC	8760
CGTCGCACTC ATTTACCCGG AGACAGGGAG AGGCTCTTCT GCGTGTAGTG GTTGTGCAGA	8820
GCCTCATGCA TCACGGAGCA TGAGAAGACG TTCCCCTGCT GCCACCTGCT CTTGTCCACG	8880
GTGAGCTTGC TGTAGAGGAA GAAGGAGCCG TCGGAGTCCA GCACGGGAGG CGTGGTCTTG	8940

TAGTTGTTCT	CCGGCTGCCC	ATTGCTCTCC	CACTCCACGG	CGATGTCGCT	GGGATAGAAG	9000
CCTTTGACCA	GGCAGGTCAG	GCTGACCTGG	TTCTTGGTCA	GCTCATCCCC	GGATGGGGGC	9060
AGGGTGTACA	CCTGTGGTTC	TCGGGGCTGC	CCTGTAGGGA	CAGAGGTTGG	TACAGCGGTC	9120
ACTCTCAGGG	CAGAGGGTGG	GCCGAGCCGG	CCTCTGTCCA	TGTGGCCCTC	GCACCCACG	9180
GGTCCCACCT	TTGGCTTTGG	AGATGGTTTT	CTCGATGGGG	GCTGGGAGGG	CTTTGTTGGA	9240
GACCTTGAC	TTGTACTCCT	TGCCATTGAG	CCAGTCCTGG	TGCAGGACGG	TGAGGACGCT	9300
GACCACACGG	TACGTGCTGT	TGTACTGCTC	CTCCCGCGGC	TTTGTCTTGG	CATTATGCAC	9360
CTCCACGCCG	TCCACGTACC	AGTTGAACTT	GACCTCAGGG	TCTTCGTGGC	TCACGTCCAC	9420
CACCACGCAT	GTGACCTCAG	GGGTCCGGGA	GATCATGAGG	GTGTCCTTGG	GTTTTGGGGG	9480
GAAGAGGAAG	ACTGATGGTC	CTCCCGCGGC	CTCAGGTGCT	GAGGGAGAGA	TGGAGGTGGA	9540
CGTGTGAGCA	CCCGGCTGGG	GCCTGTCCCT	GGATGCAGGC	TACTCTAGGG	CACCTGTCCC	9600
GCCTTGAGCT	GGAGGGCGAG	GCCTGGGCTG	GCTTACCTGG	GCACGGTGGG	CATGTGTGAG	9660
TTTTGTGACA	AGATTTGGGC	TCTGCAGAGA	GAAGATTGGG	AGTTACTCGA	ATCTGGGAGG	9720
AGAGAAGGTG	TCCGAGCTGA	GGGAGTGGAG	AGTTTGGCCT	TTGGGGTGGG	CTTAGGTCAG	9780
GGGCAGGGTC	CTCCCGGATA	TGGCTCTTGG	CAGGTCTGAG	CCCAGCACCT	GCCCCTTTGT	9840
GTGCAGGGCC	TGGGTTAGGG	GCACCTAGCC	TGTGCCTGCC	CAGAGCCTGG	GGAAAAAGCC	9900
AGAAGACCCT	CTCCCTGAGC	ATGAGTGGGG	CGGGCAGAGG	CCTCCGGGTG	AAGAGGCAGA	9960
CGGGGCCTGC	CTTGCTGCCC	TGGACTGGGG	CTGCATAGCC	GGGATGCGTC	CAGGCAGGAG	10020
CGCTGAGCCT	GGCTTCCAGC	AGACACCCTC	CCTCCCTGTG	CTGGCCTCTC	ACCAACTTTC	10080
TTGTCCACCT	TGGTGTGCT	GGGCTTGTGA	TTCACGTTGC	AGATGTAGGT	CTGGGTGCCC	10140
AAGCTGCTGG	AGGGCACGGT	CACCACGCTG	CTGAGGGAGT	AGAGTCCTGA	GGACTGTAGG	10200
ACAGCCGGGA	AGGTGTGCAC	GCCGCTGGTC	AGGGCGCCTG	AGTTCCACGA	CACCGTCACC	10260
GGTTCGGGGA	AGTAGTCCTT	GACCAGGCAG	CCCAGGGCCG	CTGTGCCCCC	AGAGGTGCTC	10320
TTGGAGGAGG	GTGCCAGGGG	GAAGACCGAT	GGGCCCTTGG	TGGAAGCTGA	GCTCACGATG	10380
ACCGTGTTTC	CTTTGCCCCA	GACGTCCATA	TAATAATTGT	CCTGGGGAGA	ATCATCCCAA	10440
CTATATGGCC	CCACTCTCGC	ACAATAATAA	ACAGCCGTGT	CTGCAGACCT	GAGGCTCCTC	10500

AACTCCATGT	AGGCTGTGTT	CGCGGATGTG	TCCGCGGTAA	AGGTGACTCT	GTCCTGGAAC	10560
TTCGCTGAAA	ATTCTTTGTT	TCCGTTGTAA	GGATTGATCC	ATCCCATCCA	CTCAAACCTC	10620
TGTCCGGGGG	CCTGGCGCAC	CCAATGAATA	ACAAAGTTAC	TGAATCTGTA	TCCAGAAGCC	10680
TGACAAGAAA	CCTTCACTGA	GGCCCCAGGC	TTCTTCACCT	CAGCCCCGGA	CTGAACCAGC	10740
TGAACCTGGG	AGTGGACACC	TGTAGTTACT	GACAGGAAGA	AGAGAAAGAC	CCAGCTCCAT	10800
TCCATGGTGG	CGGCGAATTC	GAGCTCGCCC	GGGGATCGAT	CCTCTAGAGT	CGATCGACCT	10860
GCAGCCCAAG	CTTCGTGTCA	AGGACGGTGA	CTGCAGAAAA	GACCCATGGA	AAGGAACAGT	10920
CTGTTAGTCT	GTCAGCTATT	ATGTCTGGTG	GCGCGCGCGG	CAGCAACGAG	TACTGCTCAG	10980
ACTACACTGC	CCTCCACCGT	TAACAGCACC	GCAACGGGAG	TTACCTCTGA	CTCTTATCAG	11040
AACACAACAA	CTCAGCTGCC	TGCATCTTCT	TCTGCCGCTG	CCTTAAGTCT	TCCAAATGCG	11100
TCAGCGGTGC	AAGCCCGCTC	CCCGAGCTCA	TTTTCAGACA	CATACCCTAC	CGCCACGGCC	11160
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AGGAGCAAGG	AGCTGCCGAG	CGACCATGAG	TCGCTGGAGG	CATGGGAGCA	GGGCTCGGAT	11280
GTAGAAGCTC	CGCCGCTACC	GGAGAAGAGC	CCATGTCCGG	AACACGTACC	CGAGATTGCG	11340
GTGGAGATCC	CACGTTATGT	TTAATAAAAA	CTGCGGGCAC	TGGGGACGGT	GGTGTGTGAT	11400
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TCTCTGAAGG	ACAGTGTATT	GGCATATAGC	CAATAAAGAG	AGTTGTGGCA	AAGAGCCATG	11520
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ACCCACACCT	ATAGGCTAAG	CTATACCATC	ACCTATAACA	TGAGGAAGCG	GGGGTGTATA	11640
GACCCCAAGC	CAAAAACAGT	ATAGCATGCA	TAAGAAGCCA	AGGGGGTGGG	CCTATAGACT	11700
CTATAGGCGG	TACTTACGTC	ACTCTTGGCA	CGGGGAATCC	GCGTTCCAAT	GCACCGTTCC	11760
CGGCCGCGGA	GGCTGGATCG	GTCCCGGTGT	CTTCTATGGA	GGTCAAAACA	GCGTGGATGG	11820
CGTCTCCAGG	CGATCTGACG	GTTCACTAAA	CGAGCTCTGC	TTATATAGAC	CTCCCACCGT	11880
ACACGCCTAC	CGCCCATTTG	CGTCAATGGG	GCGGAGTTGT	TACGACATTT	TGGAAAGTCC	11940
CGTTGATTTT	GGTGCCAAAA	CAAACCTCCA	TTGACGTCAA	TGGGGTGGAG	ACTTGGAAT	12000
CCCCGTGAGT	CAAACCGCTA	TCCACGCCCA	TTGATGTACT	GCCAAAACCG	CATCACCATG	12060

GTAATAGCGA	TGACTAATAC	GTAGATGTAC	TGCCAAGTAG	GAAAGTCCCA	TAAGGTCATG	12120
TACTGGGCAT	AATGCCAGGC	GGGCCATTIA	CCGTCATTGA	CGTCAATAGG	GGGCGTACTT	12180
GGCATATGAT	ACACTTGATG	TACTGCCAAG	TGGGCAGTTT	ACCGTAAATA	CTCCACCCAT	12240
TGACGTCAAT	GGAAAGTCCC	TATTGGCGTT	ACTATGGGAA	CATACGTCAT	TATTGACGTC	12300
AATGGGCGGG	GGTCGTTGGG	CGGTCAGCCA	GGCGGGCCAT	TTACCGTAAG	TTATGTAACG	12360
CGGAACTCCA	TATATGGGCT	ATGAACTAAT	GACCCCGTAA	TTGATTACTA	TTAATAACTA	12420
GTCAATAATC	AATGTCAACA	TGGCGGTAAT	GTTGGACATG	AGCCAATATA	AATGTACATA	12480
TTATGATATG	GATACAACGT	ATGCAATGGC	CAATAGCCAA	TATTGATTTA	TGCTATATAA	12540
CCAATGAATA	ATATGGCTAA	TGGCCAATAT	TGATTCAATG	TATAGATCGA	TATGCATTGG	12600
CCATGTGCCA	GCTTGATGTC	GCCTCTATCG	GCGATATAGC	CTCATATCGT	CTGTCACCTA	12660
TATCGAAACT	GCGATATTTG	CGACACACAG	AATCGCCCAA	GTCACCAAAG	TCGTCTATCG	12720
CCATCCCCCG	TAAACGATAT	AAGCGCTATC	GCCAGATATC	GCGTATGCCC	AAAAATCACT	12780
TTTGGAAGAAA	TGGCGATATC	AGTTACACAG	AAACTCACAT	CGGCGACATT	TTCAATATGC	12840
CATATTTTCA	AATATCGATT	TTTCCAATAT	CGCCATCTCT	ATCGGCGATA	AACACCACTA	12900
TCGCGCGACA	TGAATTTAGT	CGGCGACAGA	AATCTCAAAA	CGCGTATTTT	GGACAAACAC	12960
ACATTTTATT	ATTCACTGCA	GTCACCGTCC	TTGACACGAA	GCTAGAGATC	CAGACATGAT	13020
AAGATACATT	GATGAGTTTG	GACAAACCAC	AACTAGAATG	CAGTGAAAAA	AATGCTTTAT	13080
TTGTGAAATT	TGTGATGCTA	TTGCTTTTAT	TGTAACCATT	ATAAGCTGCA	ATAAACAAGT	13140
TAACAACAAC	AATTGCATTG	ATTTTATGTT	TCAGGTTTCA	GGGGAGGTGT	GGGAGGTTTT	13200
TTAAAGCAAG	TAAAACCTCT	ACAAATGTGG	TATGGCTGAT	TAATGATCAA	TGAA	13254